CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TACGTGTA 15
||||||||
Db 1 TACGTGTA 8

RESULT 508
AAF37881
ID AAF37881 standard; DNA; 10 BP.
XX
AC AAF37881;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4620.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 165; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTACAGGG 20
||||||||
Db 1 GTACAGGG 8

RESULT 509
AAF36719/c
ID AAF36719 standard; DNA; 10 BP.
XX
AC AAF36719;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3458.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 123; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCCTA 9
||||||||
Db 8 GGGCCCTA 1

RESULT 510
AAF40202/c
ID AAF40202 standard; DNA; 10 BP.
XX
AC AAF40202;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 247; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCCA 26
||||||||
Db 9 GGAGTCCA 2

RESULT 511
AAF33645
ID AAF33645 standard; DNA; 10 BP.
XX
AC AAF33645;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:384.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 389; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a

```
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTACAGGG 20
              ||||||||
Db          1 GTACAGGG 8


RESULT 512
AAF43177/c
ID   AAF43177 standard; DNA; 10 BP.
XX
AC   AAF43177;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11316.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 354; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db         10 AGTCCAGG 3


RESULT 513
ABK95857/c
ID   ABK95857 standard; DNA; 10 BP.
XX
AC   ABK95857;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #28.
XX
KW   Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW   glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW   amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200244198-A2.
XX
PD   06-JUN-2002.
XX
PF   29-NOV-2001; 2001WO-US044781.
XX
PR   30-NOV-2000; 2000US-0250254P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Kazemi A,  Russo DP,  Sausker EA;
XX
DR   WPI; 2002-519580/55.
XX
PT   Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT   Amino Acid Transporter), Member 4 isogenes, for improving efficiency and
```

PT reliability in drug development for treating cancers.
XX
PS Claim 17; Page 16; 139pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC first nucleotide sequence which comprises solute carrier family 1
CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes
CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLC1A4
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful
CC in screening for drugs targeting (III) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLC1A4 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLC1A4 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLC1A4 activity. The methods are also useful for screening compounds
CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4
CC gene allele-specific oligonucleotides, primer extension oligonucleotides
CC and related PCR primers used to identify single nucleotide polymorphisms
CC (SNP) of the gene
XX
SQ Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 ACAGGGAG 22
||||||||
Db 9 ACAGGGAG 2

RESULT 514
ABL42870/c
ID ABL42870 standard; cDNA; 10 BP.
XX
AC ABL42870;
XX
DT 12-APR-2002 (first entry)
XX
DE Human maturation/activation dendritic cell expression gene tag #244.
XX
KW Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
OS Homo sapiens.
XX
PN JP2001327293-A.
XX
PD 27-NOV-2001.
XX
PF 22-MAY-2000; 2000JP-00150562.
XX
PR 22-MAY-2000; 2000JP-00150562.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-127070/17.
XX
PT Human maturation/activation dendritic cell expression gene group.
XX
PS Claim 19; Page 16; 41pp; Japanese.
XX
CC The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention
XX
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GTGTACAG 18
||||||||
Db 9 GTGTACAG 2

RESULT 515
ABK37012
ID ABK37012 standard; DNA; 10 BP.
XX
AC ABK37012;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human ALAS2 gene allele-specific oligonucleotide PCR primer #11.
XX
KW Human; aminolevulinate delta synthase 2; ALAS2; haplotyping; primer; ss;
KW haplotype pair; single nucleotide polymorphism; genotyping; antianaemic;
KW gene therapy; drug screening; X-linked sideroblastic anaemia; sequencing;
KW hypochromic anaemia; probe; PCR.
XX
OS Homo sapiens.
XX
PN WO200210454-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US023914.
XX
PR 28-JUL-2000; 2000US-0221827P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Kliem S, Stephens JC;
XX
DR WPI; 2002-188755/24.
XX
PT New isolated human aminolevulinate delta synthase 2 polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the aminolevulinate protein.
XX
PS Claim 18; Page 14; 90pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding human aminolevulinate delta synthase 2 (ALAS2). A method for
CC haplotyping the ALAS2 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the ALAS2 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the ALAS2 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype
CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. ALAS2 and its corresponding DNA are used
CC for studying the expression and function of ALAS2, for use in screening

```
CC   for candidate drugs to treat diseases related to ALAS2 activity, such as
CC   X-linked sideroblastic anaemia and hypochromic anaemia. The sequences are
CC   also useful for studying the effect of variation on the biological
CC   activity of ALAS2 as well as on the binding affinity of candidate drugs
CC   targeting ALAS2. Sequences ABK36963-ABK37027 represent allele-specific
CC   oligonucleotide probes, sequencing primers and PCR primers used to detect
CC   ALAS2 gene polymorphisms
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
               ||||||||
Db          2 AGTCCAGG 9


RESULT 516
ABN80618/c
ID   ABN80618 standard; DNA; 10 BP.
XX
AC   ABN80618;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human P450(cytochrome) oxidoreductase ASO primer extension oligo #6.
XX
KW   Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
KW   single nucleotide polymorphism; flavoprotein; enzyme;
KW   primer extension oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226768-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-US030877.
XX
PR   29-SEP-2000; 2000US-0236449P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kazemi A,  Kliem SE,  Lanz EM,  Messer C,  Tanguay DA;
XX
DR   WPI; 2002-394236/42.
XX
PT   New genetic variants comprising haplotypes of the P450 (cytochrome)
PT   oxidoreductase (POR) isogene, useful in improving the efficiency of drug
PT   screening protocols for compounds targeting POR.
XX
PS   Claim 16; Page 15; 141pp; English.
XX
CC   The present invention provides the protein, gene and cDNA sequences of
CC   human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC   polymorphisms (SNPs) identified therein. The sequences can be used to
CC   haplotype the POR gene of an individual, and to establish whether POR is
CC   a suitable target for drugs to treat cancer and disorders associated with
CC   impaired protein synthesis in cells. The present sequence is an allele
CC   specific primer extension oligonucleotide for the coding sequences of the
CC   invention
XX
SQ   Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGT 23
               ||||||||
Db          8 CAGGGAGT 1


RESULT 517
ABV84803
ID   ABV84803 standard; cDNA; 10 BP.
XX
AC   ABV84803;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human S-protein/somatomedin B/vitronectin SAGE tag #613.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 55; Page 28; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
CC   expressed in chronic hepatitis C liver tissue
XX
SQ   Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
               ||||||||
Db          3 CGGGCCCT 10


RESULT 518
ABV84905
ID   ABV84905 standard; cDNA; 10 BP.
XX
AC   ABV84905;
XX
DT   12-DEC-2002  (first entry)
```

XX
DE Human S-protein/somatomedin B/vitronectin SAGE tag #715.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-00012328.
XX
PR 19-JAN-2001; 2001JP-00012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
PT Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
XX
PS Claim 64; Page 30; 139pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC expressed in hepatocellular carcinoma
XX
SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

```
  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10
```

RESULT 519
ABK23745/c
ID ABK23745 standard; DNA; 10 BP.
XX
AC ABK23745;
XX
DT 09-APR-2002 (first entry)
XX
DE Transcript tag DNA sequence #334 induced or suppressed by N-myc.
XX
KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN WO200185941-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-NL000361.
XX
PR 11-MAY-2000; 2000EP-00201698.
PR 29-JUN-2000; 2000EP-00202284.
XX
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI Versteeg R, Caron HN;
XX
DR WPI; 2002-066603/09.
XX
PT A new nucleic acid library of myc-dependent downstream genes capable of
PT supporting a neoplastic characteristic of cancer is useful to find new
PT therapies and diagnoses for cancer.
XX
PS Disclosure; Page 58; 69pp; English.
XX
CC The present invention relates to a nucleic acid library comprising myc-
CC dependent downstream genes or their functional fragments essentially
CC capable of supporting a neoplastic character of cancer such as growth,
CC invasion or spread. These myc target or tag sequences are identified by
CC SAGE (serial analysis of gene expression). The library is useful to find
CC new diagnoses and treatments for cancer. The invention is also useful to
CC enhance production of recombinant proteins in a production system with
CC high expression of endogenous or transfected myc oncogenes. ABK23412-
CC ABK23828 represent transcript tag DNA sequences that are activated or
CC repressed by N-myc in human neuroblastoma
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

```
  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3
```

RESULT 520
AAS16755
ID AAS16755 standard; DNA; 10 BP.
XX
AC AAS16755;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human APOA4 ASO, primer extension primer #8 terminal sequence.
XX
KW Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
KW atherosclerosis; PCR primer; primer extension.
XX
OS Homo sapiens.
XX
PN WO200177124-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010670.
XX
PR 05-APR-2000; 2000US-0194362P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;
XX
DR WPI; 2002-041281/05.
XX

PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
PT and treat disorders associated with its abnormal expression or function
PT such as coronary artery disease.
XX
PS Claim 17; Page 15; 71pp; English.
XX
CC The invention relates to haplotyping the human apolipoprotein A-IV
CC (APOA4) gene of an individual, comprising determining if the individual
CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
CC specification. Also disclosed are genotyping oligonucleotides (or allele
CC specific oligonucleotides, ASO) as well as methods for correlating a
CC particular haplotype pair with a trait e.g. obesity, in a population. The
CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
CC invention are useful to diagnose and develop treatment for disorders
CC associated with abnormal APOA4 expression or function, for example
CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
CC screened compounds are useful for the treatment of disorders associated
CC with abnormal APOA4 expression or function such as coronary artery
CC disease. The present sequence is the terminus of an APOA4 allele specific
CC oligonucleotide, ASO, primer extension PCR primer used to detect an APOA4
CC polymorphism
XX
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
||||||||
Db 1 CGGGCCCT 8

RESULT 521
AAS16821/c
ID AAS16821 standard; DNA; 10 BP.
XX
AC AAS16821;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human apolipoprotein C1 (APOC1) gene PCR primer #7.
XX
KW Human; apolipoprotein C1; APOC1; single nucleotide polymorphism;
KW haplotyping; haplotype pair; hypercholesterolaemia; nootropic; SDAT; ss;
KW senile dementia of Alzheimer's type; neuroprotective; antilipaemic;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200177129-A2.
XX
PD 18-OCT-2001.
XX
PF 10-APR-2001; 2001WO-US011808.
XX
PR 11-APR-2000; 2000US-0196545P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;
XX
DR WPI; 2002-041286/05.
XX
PT New haplotypes of the human apolipoprotein C1 gene, useful to detect and
PT find treatment for disease associated with its activity such as
PT hypercholestrolemia and Alzheimer's disease.
XX
PS Claim 18; Page 13; 51pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the human
CC apolipoprotein C1 (APOC1) gene. Haplotyping the APOC1 gene of an
CC individual, comprises determining if the individual has one of the APOC1
CC haplotypes or haplotype pairs fully defined in the specification.
CC Genotyping the APOC1 gene of an individual, comprises determining the
CC identity of the nucleotide pair at one or more polymorphic sites and
CC predicting a haplotype pair for the APOC1 gene of an individual by
CC enumerating all possible haplotype pairs which are consistent with the
CC genotype, comparing the possible haplotype pairs to the data detailed in
CC the specification and assigning a haplotype pair to the individual that
CC is consistent with the data. Identifying an association between a trait
CC and a haplotype or haplotype pair of the APOC1 gene, comprises comparing
CC the frequency of the haplotype/haplotype pair in a population exhibiting
CC the trait with that of a reference population, where the
CC haplotype/haplotype pair is one described in the specification and a
CC higher frequency in the trait population indicates the trait is
CC associated with the haplotype. The sequences and methods of the invention
CC are used to diagnose and develop treatment for disease associated with
CC APOC1 activity, such as hypercholesterolaemia and senile dementia of
CC Alzheimer's type (SDAT). This sequence represents a PCR primer used for
CC detecting human APOC1 DNA polymorphisms
XX
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GGGAGTCC 25
||||||||
Db 10 GGGAGTCC 3

RESULT 522
AAS95473
ID AAS95473 standard; DNA; 10 BP.
XX
AC AAS95473;
XX
DT 14-FEB-2002 (first entry)
XX
DE Interleukin 5 (IL5) allele-specific oligonucleotide #31.
XX
KW Human; allele-specific oligonucleotide; ASO; interleukin 5; IL5;
KW antiinflammatory; antiasthmatic; haplotyping; inflammatory disorder;
KW asthma; ss.
XX
OS Homo sapiens.
XX
PN WO200177132-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US012011.
XX
PR 11-APR-2000; 2000US-0196250P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;
PI Nandabalan K, Parks KE;
XX
DR WPI; 2002-041289/05.
XX
PT New haplotypes of the human interleukin 5 gene, useful to diagnose and
PT treat diseases associated with the gene including inflammatory disorders
PT such as asthma.
XX
PS Claim 17; Page 13; 65pp; English.
XX
CC The invention relates to haplotyping the human interleukin 5 (IL5) gene
CC of an individual, comprising determining if the individual has one of the
CC IL5 haplotypes or haplotype pairs fully defined in the specification.
CC Haplotyping the IL5 gene of an individual, comprises determining the
CC identity of the nucleotide at two or more polymorphic sites in one copy
CC of the gene. The method also involves identifying an association between

CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising
CC comparing the frequency of the haplotype/pair in a population exhibiting
CC the trait with that of a reference population. A higher frequency in the
CC trait population indicates the trait is associated with the haplotype.
CC The polynucleotides and screened compounds are useful to develop
CC treatment for diseases associated with IL-5 activity including
CC inflammatory disorders such as asthma. AAS95443-AAS95489 represent IL5
CC allele-specific oligonucleotides (ASO) and PCR primers of the invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGTCCAGG 28
||||||||
Db 1 AGTCCAGG 8

RESULT 523
AAS99418
ID AAS99418 standard; DNA; 10 BP.
XX
AC AAS99418;
XX
DT 12-MAR-2002 (first entry)
XX
DE Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #111.
XX
KW Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
KW succinate-semialdehyde dehydrogenase; gene therapy; primer;
KW antisense technology; primer extension oligonucleotide;
KW 4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.
XX
OS Synthetic.
XX
PN WO200190119-A2.
XX
PD 29-NOV-2001.
XX
PF 21-MAY-2001; 2001WO-US016558.
XX
PR 19-MAY-2000; 2000US-0205849P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kliem SE, Koshy B, Tanguay DA;
XX
DR WPI; 2002-089912/12.
XX
PT New genetic variants of human aldehyde dehydrogenase 5 family, member A1,
PT ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1
PT protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.
XX
PS Claim 18; Page 15; 151pp; English.
XX
CC The invention describes an isolated polynucleotide comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for the aldehyde dehydrogenase 5 family, member A1 (succinate-
CC semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment. The
CC polypeptide is useful for screening for drugs targeting it by contacting
CC the ALDH5A1 polymorphic variant with a candidate agent and assaying for
CC binding activity. The polypeptide and haplotypes are useful for
CC identifying an association between a trait such as a clinical response to
CC a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene. Transgenic animals
CC are also useful for studying expression of the ALDH5A1 isogenes in vivo,
CC for in vivo screening and testing of drugs against ALDH5A1 protein and
CC for testing the efficacy of therapeutic agents and compounds for 4-
CC hydroxybutyric aciduria and metabolic diseases in a biological system.
CC Antibodies are useful for diagnostic and prognostic formats and
CC therapeutic methods, for immunoprecipitating the polypeptide from
CC solution, for detecting ALDH5A1 protein isoforms in biological samples,
CC frozen tissue sections, for use in immunocytochemical,
CC immunohistochemical and immunofluorescence techniques. The polynucleotide
CC is useful for gene therapy and antisense gene therapy. This sequence is a
CC primer extension oligonucleotide used to detect polymorphisms in the
CC ALDH5A1 gene described in the method of the invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 ACAGGGAG 22
||||||||
Db 1 ACAGGGAG 8

RESULT 524
AAD51664/c
ID AAD51664 standard; DNA; 10 BP.
XX
AC AAD51664;
XX
DT 16-APR-2003 (first entry)
XX
DE Human CYP2E gene polymorphism detecting primer #13.
XX
KW Human; cytochrome P450 subfamily IIE; CYP2E protein; haplotyping;
KW genotyping; gene therapy; cancer; polymorphism; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200290597-A1.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-US014540.
XX
PR 07-MAY-2001; 2001US-0289330P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Gilson CR, Koshy B, Sausker EA;
XX
DR WPI; 2003-120563/11.
XX
PT New genetic variants comprising haplotypes of the cytochrome P450,
PT subfamily IIE (CYP2E) gene, useful for screening drugs for treating
PT cancer, validating CYP2E protein as a drug target, or reducing bias in
PT clinical trials of such drugs.
XX
PS Claim 39; Page 16; 94pp; English.
XX
CC The invention relates to genetic variants of human cytochrome P450,
CC subfamily IIE (CYP2E) gene. The invention also relates to compositions
CC and methods for haplotyping and/or genotyping the CYP2E gene in an
CC individual. The polynucleotide comprising polymorphisms in the CYP2E gene
CC are useful in screening candidate drugs to treat diseases related to
CC CYP2E activity, e.g. cancer. The methods and haplotypes are useful in
CC improving the efficiency of drug discovery and development processes, or
CC for designing clinical trials of candidate drugs for treating the
CC specific condition or disease. The polymorphisms and haplotypes of CYP2E
CC gene are useful for validating whether CYP2E is a suitable target for
CC drugs to treat cancer and disorders associated with impaired protein
CC synthesis in cells, screening for drugs and reducing bias in clinical
CC trials of the drugs. The invention is also useful in gene therapy. The
CC present sequence is a primer used to detect human CYP2E gene
CC polymorphisms
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db          9 GAGTCCAG 2


RESULT 525
AAA74982/c
ID   AAA74982 standard; DNA; 11 BP.
XX
AC   AAA74982;
XX
DT   02-JAN-2001  (first entry)
XX
DE   Nucleotide sequence of a copy of a polymerase template.
XX
KW   Morpholine nucleotide analogue; DNA labelling; chain terminator;
KW   nucleic acid sequencing; ss.
XX
OS   Synthetic.
XX
PN   FR2790005-A1.
XX
PD   25-AUG-2000.
XX
PF   27-SEP-1999;   99FR-00012001.
XX
PR   22-FEB-1999;   99FR-00002170.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI   Marciacq F,  Sauvaigo S,  Mouret JF,  Issartel JP,  Molko D;
XX
DR   WPI; 2000-589230/56.
XX
PT   Use of new and known morpholine nucleotide analogs for labeling nucleic
PT   acid fragments, especially for nucleic acid sequencing.
XX
PS   Disclosure; Page 5; 68pp; French.
XX
CC   The specification describes morpholine nucleotide analogue, which are
CC   used for labelling DNA or RNA fragments. The morpholine nucleotide
CC   analogues are useful as chain terminators for the enzymatic synthesis of
CC   3'-labelled complementary strands during nucleic acid sequencing. The
CC   present sequence represents a copy of the polymerase template (given in
CC   AAA74965), which is produced the method of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGT 12
              :||| |||||
Db         11 SGCCTTACGT 2


RESULT 526
AAZ39365
ID   AAZ39365 standard; DNA; 11 BP.
XX
AC   AAZ39365;
XX
DT   23-FEB-2000  (first entry)
XX
DE   Mutant tat HIV retroviral vectors constructing PCR muatgenesis primer.
XX
KW   HIV; 293 cell line; TAR mutant virus; transactivator protein; TAR virus;
KW   mutation; Tat protein; viral regulatory protein; vaccine; mutagenesis;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Human immunodeficiency virus 1.
XX
PN   US5994108-A.
XX
PD   30-NOV-1999.
XX
PF   05-AUG-1994;   94US-00286874.
XX
PR   05-NOV-1991;   91US-00788266.
PR   02-JUL-1992;   92US-00910867.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Gaynor RB,  Harrich D;
XX
DR   WPI; 2000-052344/04.
XX
PT   293 cell line for producing wild-type levels of HIV TAR mutant virus.
XX
PS   Example 11; Col 36; 61pp; English.
XX
CC   The invention provides a 293 cell line that produces wild-type levels of
CC   HIV TAR mutant virus in the presence of a transactivator protein, the
CC   cell line being infected with a mutant HIV TAR virus having a mutation in
CC   the loop sequence on the bulge sequence. The cell line is useful for
CC   producing wild-type levels of HIV TAR mutant virus which encode mutant
CC   Tat proteins (viral regulatory proteins) which are capable of inhibiting
CC   the expression of the HIV-1 virus in the presence of an equimolar
CC   concentration of the wild-type Tat protein. Sequences AAZ39364-67
CC   represent PCR mutagenesis primers used in the construcction of mutant tat
CC   HIV retroviral vectors
XX
SQ   Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTA 9
              ||||||||
Db          1 GGGCCCTA 8


RESULT 527
AAA74965/c
ID   AAA74965 standard; DNA; 11 BP.
XX
AC   AAA74965;
XX
DT   02-JAN-2001  (first entry)
XX
DE   Nucleotide sequence of a copy of a polymerase template.
XX
KW   Morpholine nucleotide analogue; DNA labelling; chain terminator;
KW   nucleic acid sequencing; ss.
XX
OS   Synthetic.
XX
PN   FR2790004-A1.
XX
PD   25-AUG-2000.
XX
PF   22-FEB-1999;   99FR-00002170.
XX
PR   22-FEB-1999;   99FR-00002170.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI   Marciacq F,  Sauvaigo S,  Mouret JF,  Issartel JP,  Molko D;
XX
DR   WPI; 2000-589229/56.
XX
```

```
PT   Use of new and known morpholine nucleotide analogs for labeling nucleic
PT   acid fragments, especially for nucleic acid sequencing.
XX
PS   Disclosure; Page 5; 51pp; French.
XX
CC   The specification describes morpholine nucleotide analogue, which are
CC   used for labelling DNA or RNA fragments. The morpholine nucleotide
CC   analogues are useful as chain terminators for the enzymatic synthesis of
CC   3'-labelled complementary strands during nucleic acid sequencing. The
CC   present sequence represents a copy of the polymerase template (given in
CC   AAA74965), which is produced the method of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGT 12
              :||| |||||
Db         11 SGCCTTACGT 2


RESULT 528
ABQ87185
ID   ABQ87185 standard; cDNA; 11 BP.
XX
AC   ABQ87185;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 940.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 76; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCC 25
              ||||||||
Db          4 GGGAGTCC 11


RESULT 529
ABQ87673
ID   ABQ87673 standard; cDNA; 11 BP.
XX
AC   ABQ87673;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1428.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 98; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          3 GGAGTCCA 10


RESULT 530
ABQ86610
ID   ABQ86610 standard; cDNA; 11 BP.
XX
AC   ABQ86610;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 365.
```

```
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 51; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          2 GGAGTCCA 9


RESULT 531
ABQ86755/c
ID   ABQ86755 standard; cDNA; 11 BP.
XX
AC   ABQ86755;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 510.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 58; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db         11 GAGTCCAG 4


RESULT 532
ABQ86291/c
ID   ABQ86291 standard; cDNA; 11 BP.
XX
AC   ABQ86291;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 46.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 39; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
```

```
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          21 AGTCCAGG 28
               ||||||||
Db          10 AGTCCAGG 3


RESULT 533
ABV68516/c
ID   ABV68516 standard; cDNA; 11 BP.
XX
AC   ABV68516;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6302.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 200; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAG 22
               ||||||||
Db          11 ACAGGGAG 4


RESULT 534
ABV68894
ID   ABV68894 standard; cDNA; 11 BP.
XX
AC   ABV68894;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6680.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 211; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCA 26
               ||||||||
Db           2 GGAGTCCA 9


RESULT 535
ABV70231/c
ID   ABV70231 standard; cDNA; 11 BP.
XX
AC   ABV70231;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8017.
XX
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KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 255; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          21 AGTCCAGG 28
               ||||||||
Db          11 AGTCCAGG 4


RESULT 536
ABV71814/c
ID   ABV71814 standard; cDNA; 11 BP.
XX
AC   ABV71814;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9600.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 310; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GAGTCCAG 27
               ||||||||
Db          11 GAGTCCAG 4


RESULT 537
ABV62315
ID   ABV62315 standard; cDNA; 11 BP.
XX
AC   ABV62315;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 101.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 28; 1345pp; German.
XX
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```
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAG 22
              ||||||||
Db          2 ACAGGGAG 9


RESULT 538
ABV67037/c
ID   ABV67037 standard; cDNA; 11 BP.
XX
AC   ABV67037;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4823.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 158; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db         10 AGTCCAGG 3


RESULT 539
ABV70819
ID   ABV70819 standard; cDNA; 11 BP.
XX
AC   ABV70819;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8605.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 275; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGG 19
              ||||||||
Db          4 TGTACAGG 11


RESULT 540
ABV64705
```

ID ABV64705 standard; cDNA; 11 BP.
XX
AC ABV64705;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2491.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 94; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCCTACG 11
||||||||
Db 4 GCCCTACG 11

RESULT 541
ABV62810/c
ID ABV62810 standard; cDNA; 11 BP.
XX
AC ABV62810;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 596.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 41; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGTCCAGG 28
||||||||
Db 11 AGTCCAGG 4

RESULT 542
ABV64719/c
ID ABV64719 standard; cDNA; 11 BP.
XX
AC ABV64719;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2505.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX

```
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 94; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTA 9
              ||||||||
Db          9 GGGCCCTA 2


RESULT 543
ABV65110
ID   ABV65110 standard; cDNA; 11 BP.
XX
AC   ABV65110;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2896.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 105; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db          4 GAGTCCAG 11


RESULT 544
ABV71864/c
ID   ABV71864 standard; cDNA; 11 BP.
XX
AC   ABV71864;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9650.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 312; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          7 CTACGTGT 14
              ||||||||
Db         11 CTACGTGT 4


RESULT 545
ABV65919
ID   ABV65919 standard; cDNA; 11 BP.
XX
AC   ABV65919;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3705.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 128; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCC 25
              ||||||||
Db          4 GGGAGTCC 11


RESULT 546
ABV63398
ID   ABV63398 standard; cDNA; 11 BP.
XX
AC   ABV63398;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1184.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 57; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGG 19
              ||||||||
Db          4 TGTACAGG 11


RESULT 547
ABV64393/c
ID   ABV64393 standard; cDNA; 11 BP.
XX
AC   ABV64393;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2179.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
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PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 85; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GAGTCCAG 27
               ||||||||
Db          11 GAGTCCAG 4


RESULT 548
ABV64443/c
ID   ABV64443 standard; cDNA; 11 BP.
XX
AC   ABV64443;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2229.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 87; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           7 CTACGTGT 14
                 ||||||||
Db          11 CTACGTGT 4


RESULT 549
ABV72049
ID   ABV72049 standard; cDNA; 11 BP.
XX
AC   ABV72049;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9835.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 319; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
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```
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          3 GGAGTCCA 10


RESULT 550
ABV69736
ID   ABV69736 standard; cDNA; 11 BP.
XX
AC   ABV69736;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7522.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 237; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAG 22
              ||||||||
Db          2 ACAGGGAG 9


RESULT 551
ABV66268
ID   ABV66268 standard; cDNA; 11 BP.
XX
AC   ABV66268;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4054.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 137; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTA 9
              ||||||||
Db          3 GGGCCCTA 10


RESULT 552
ABV68998/c
ID   ABV68998 standard; cDNA; 11 BP.
XX
AC   ABV68998;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6784.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
```

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 213; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GAGTCCAG 27
||||||||
Db 9 GAGTCCAG 2

RESULT 553
ABL91942
ID ABL91942 standard; cDNA; 11 BP.
XX
AC ABL91942;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Pan-Endothelial Marker SEQ ID NO 40.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2002-291856/33.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Example 4; Page 325; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995. The present sequence is that of an
CC oligonucleotide marker useful to the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCCCTAC 10
||||||||
Db 1 GGCCCTAC 8

RESULT 554
ABK68760/c
ID ABK68760 standard; DNA; 11 BP.
XX
AC ABK68760;
XX
DT 02-JUL-2002 (first entry)
XX
DE Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
XX
KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200218641-A2.
XX
PD 07-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-IB001580.
XX
PR 30-AUG-2000; 2000GB-00021286.
XX
PA (GEMI-) GEMINI GENOMICS PLC.
XX
PI Risinger C, Andersson MK, Lewander T, Olaisson E;
XX
DR WPI; 2002-351712/38.
XX
PT Novel primer pairs and sequence determination oligonucleotides useful for
PT amplifying and detecting novel single nucleotide polymorphisms in the 5'
PT flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes

PT respectively.
XX
PS Claim 4; Page 17; 47pp; English.
XX
CC The present invention relates to PCR primer pairs for amplifying and
CC sequence determination oligonucleotides for detecting single nucleotide
CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
CC The PCR primers are useful for amplifying the CYP sequences and the
CC oligonucleotides are useful for detecting SNPs in the 5'-flanking regions
CC of the CYP3A4 or CYP2C9 genes. ABK68755-ABK68761 represent
CC oligonucleotides for detecting the polymorphism in the 5'-flanking region
CC of the human CYP3A4 gene
XX
SQ Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GTGTACAG 18
||||||||
Db 9 GTGTACAG 2

RESULT 555
ABK68759
ID ABK68759 standard; DNA; 11 BP.
XX
AC ABK68759;
XX
DT 02-JUL-2002 (first entry)
XX
DE Oligonucleotide #5 for detecting SNP in 5'-region of human CYP3A4 gene.
XX
KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200218641-A2.
XX
PD 07-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-IB001580.
XX
PR 30-AUG-2000; 2000GB-00021286.
XX
PA (GEMI-) GEMINI GENOMICS PLC.
XX
PI Risinger C, Andersson MK, Lewander T, Olaisson E;
XX
DR WPI; 2002-351712/38.
XX
PT Novel primer pairs and sequence determination oligonucleotides useful for
PT amplifying and detecting novel single nucleotide polymorphisms in the 5'
PT flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
PT respectively.
XX
PS Claim 4; Page 17; 47pp; English.
XX
CC The present invention relates to PCR primer pairs for amplifying and
CC sequence determination oligonucleotides for detecting single nucleotide
CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
CC The PCR primers are useful for amplifying the CYP sequences and the
CC oligonucleotides are useful for detecting SNPs in the 5'-flanking regions
CC of the CYP3A4 or CYP2C9 genes. ABK68755-ABK68761 represent
CC oligonucleotides for detecting the polymorphism in the 5'-flanking region
CC of the human CYP3A4 gene
XX
SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GTGTACAG 18
||||||||
Db 3 GTGTACAG 10

RESULT 556
ABL51577/c
ID ABL51577 standard; DNA; 11 BP.
XX
AC ABL51577;
XX
DT 03-JUL-2002 (first entry)
XX
DE Transferrin receptor gene related oligonucleotide fragment #7.
XX
KW Polymorphism; single nucleotide polymorphism; SNP; identification;
KW detection; hybridisation; genotyping; transferrin receptor; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200221098-A2.
XX
PD 14-MAR-2002.
XX
PF 04-SEP-2001; 2001WO-US027446.
XX
PR 05-SEP-2000; 2000US-00655104.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Stanton VP, Wolfe JL, Kawate T, Verdine GL;
XX
DR WPI; 2002-362259/39.
XX
PT Detecting polymorphism in a polynucleotide (N) comprises hybridizing an
PT oligonucleotide with a variant (N) having modified nucleotides
PT incorporated at each point of suspected polymorphism occurrence.
XX
PS Example 4; Fig 29b; 245pp; English.
XX
CC The present invention describes a method for detecting a polymorphism (P)
CC in polynucleotide (N). The method comprises: (1) hybridising
CC oligonucleotides with fragments of (N) segments which contain a
CC polymorphism, and have modified nucleotides that are incorporated at each
CC point of occurrence of suspected (P) during amplification; and (2)
CC analysing the hybridising fragments for an incorporated detectable label
CC identifying the susceptible polymorphism. The method is used for
CC detecting polymorphisms (e.g. a single nucleotide polymorphism (SNP), a
CC deletion or a insertion) in (N). The method is useful for developing
CC diagnostic and prognostic tools for detecting a predisposition of certain
CC disease and disorders. The method is useful for detecting variance in DNA
CC sequencing, and has applications in genotyping. The present sequence
CC represents a transferrin receptor gene related oligonucleotide sequence,
CC which is used in an example from the present invention
XX
SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 ACAGGGAG 22
||||||||
Db 11 ACAGGGAG 4

```
RESULT 557
ABX71867
ID   ABX71867 standard; DNA; 11 BP.
XX
AC   ABX71867;
XX
DT   12-MAR-2003  (first entry)
XX
DE   DNA tag used to identify human gene encoding PEM 40.
XX
KW   Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW   Tumour endothelial marker; normal endothelial marker; PEM;
KW   pan-endothelial marker; polycystic kidney disease; psoriasis;
KW   diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW   neoangiogenesis; immune response; cytostatic; antidiabetic;
KW   ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200283874-A2.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-US008253.
XX
PR   11-APR-2001; 2001US-0282850P.
PR   06-FEB-2002; 2002US-0354262P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Carson-Walter E,  St Croix B,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2003-093016/08.
XX
PT   New purified human transmembrane protein, designated as tumor endothelial
PT   marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT   polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT   psoriasis.
XX
PS   Disclosure; Page 93; 374pp; English.
XX
CC   The present invention relates to a novel method for the isolation of
CC   endothelial cells (ECs), and the identification of genes expressed in
CC   normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC   endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC   identified in human ECs. The human EC marker proteins and the
CC   polynucleotide sequences encoding them are useful for detecting,
CC   diagnosing or treating tumours as well as polycystic kidney disease,
CC   diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC   useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC   inducing an immune response to tumour endothelial cells in a patient, or
CC   for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC   represent DNA tags for human PEM, TEM or NEM genes
XX
SQ   Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTAC 10
              ||||||||
Db          1 GGCCCTAC 8


RESULT 558
AAX79373
ID   AAX79373 standard; DNA; 12 BP.
XX
AC   AAX79373;
XX
DT   17-AUG-1999  (first entry)
XX
DE   HLA-DR typing probe L74.
XX
KW   Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
KW   major histocompatibility complex; bone marrow transplant; primer;
KW   amplification; polymerase chain reaction; probe; polymorphism;
KW   sequence-specific oligonucleotide probe hybridisation; ss.
XX
OS   Synthetic.
XX
PN   US5468611-A.
XX
PD   21-NOV-1995.
XX
PF   08-APR-1993;   93US-00045530.
XX
PR   27-JUN-1990;   90US-00544218.
XX
PA   (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI   Gorski JA,  Baxter-Lowe LA;
XX
DR   WPI; 1996-010091/01.
XX
PT   Improved method for HLA typing - by DNA amplification and sequence-
PT   specific oligo:nucleotide hybridisation, used to select bone marrow
PT   donors.
XX
PS   Disclosure; Col 19-20; 20pp; English.
XX
CC   A novel method of typing the human leukocyte antigen (HLA) of the major
CC   histocompatibility complex (MHC), esp. for typing donors for bone marrow
CC   transplants, involves determining if the donor tissue HLA-DR alleles are
CC   selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1, DR6a,
CC   DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-
CC   c. The method uses PCR to amplify these regions followed by sequence-
CC   specific oligonucleotide probe hybridisation (SSOPH) using the probes
CC   AAX79365-X79429. SSOPH allows detection of polymorphisms that predict
CC   differences at a single amino acid level thus reducing errors and
CC   improving the chance of successfully matching tissues
XX
SQ   Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          4 CGGGCCCT 11


RESULT 559
AAT41818/c
ID   AAT41818 standard; DNA; 12 BP.
XX
AC   AAT41818;
XX
DT   25-MAR-2003  (revised)
DT   18-DEC-1996  (first entry)
XX
DE   HLA allele, HLA-DRB1*08, *12 and *1404 resolution probe, L74.
XX
KW   Human leukocyte antigen; HLA; allele; HLA-DR*08; HLA-DR*12; locus B1;
KW   polymorphism; amplify; conserved region; detection; primer; probe;
KW   tissue matching; identifying disease susceptibility; ss.
XX
OS   Synthetic.
XX
PN   US5545526-A.
XX
PD   13-AUG-1996.
```

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XX
PF   01-MAR-1993;   93US-00025038.
XX
PR   27-JUN-1990;   90US-00544218.
XX
PA   (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI   Baxter-Lowe LA;
XX
DR   WPI; 1996-383664/38.
XX
PT   Human leukocyte antigen typing of tissue samples - using allele-specific
PT   amplification to distinguish allele pairs.
XX
PS   Example 1; Col 19; 24pp; English.
XX
CC   The sequences given in AAT41811-20 represent probes which were used to
CC   resolve the human leukocyte antigen (HLA) DRB1 alleles, DRB1*08, *12 and
CC   *1404. This probe sequence hybridises to the Leu74 coding region found in
CC   alleles *0801, *0802, *0803 and 0804. These probes may be used in the
CC   method of invention which concerns HLA typing of a sample for an unknown
CC   pair of alleles. The pair of alleles comprises one of two known types
CC   which have the same overall set of polymorphisms but have a different
CC   distribution of polymorphisms between their two alleles. The method
CC   comprises selectively amplifying the DNA of just one allele of the
CC   unknown pair and analysing the amplified DNA to determine which
CC   polymorphisms are present in that allele, and therefore assigning the
CC   unknown pair to the known type having that allele. The method comprises
CC   three test stages. The first stage is to establish the number of alleles
CC   present in each sample. Primers corresponding to fairly well conserved
CC   regions of a locus will increase the likelihood that unknown alleles will
CC   be amplified and potentially detected by hybridisation with a probe. In
CC   the second stage, the group or basic type identified determines which set
CC   of allele specific primers will be used. The first of the two primers
CC   comprises an opt. labeled sequence common to each allele of the group
CC   identified in the first stage but different from other groups identified
CC   in stage one. The second primer may be a mixture of different labeled
CC   primers, complementary to two or more sequences within the group, or the
CC   amplification may be performed with only one second primer to detect the
CC   presence of a single group of alleles. In the third stage the specific
CC   allele is determined. This may be done by amplification or hybridisation
CC   using a radiolabelled probe. The method may be used for tissue matching,
CC   identifying disease susceptibility, etc. The method of the invention esp.
CC   distinguishes between DQB1*0304/DQB1*03032 and DQB1*0301/DQB1*0302.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 12 BP; 1 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 560
AAV16569
ID   AAV16569 standard; DNA; 12 BP.
XX
AC   AAV16569;
XX
DT   12-JUN-1998  (first entry)
XX
DE   Probe L74 used to identify HLA-DR sequences.
XX
KW   DR region; major histocompatibility complex; HLA-DR; HLA-typing;
KW   HLA-DR beta consensus sequence; allelic polymorphism;
KW   HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5702885-A.
XX
PD   30-DEC-1997.
XX
PF   08-APR-1993;   93US-00057957.
XX
PR   27-JUN-1990;   90US-00544218.
XX
PA   (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI   Gorski JA,  Baxter-Lowe LA;
XX
DR   WPI; 1998-076408/07.
XX
PT   Oligo:nucleotide probes and primers and methods for HLA typing -
PT   particularly for tissue typing for bone marrow transplants.
XX
PS   Disclosure; Col 19; 20pp; English.
XX
CC   Probes AAV16561-624 are used to identify differences in the DR region of
CC   human major histocompatibility complex (HLA-DR). The specification
CC   describes a method for HLA-typing, which includes an oligonucleotide
CC   probe which undergoes sequence-specific hybridisation with an HLA-DR beta
CC   consensus sequence at positions 61-64. The probe contains a labelling
CC   substance other than a nucleotide sequence, which facilitates detection
CC   of the probe. The HLA sequence of a subject is PCR amplified, and a probe
CC   that recognises an allelic polymorphism at a selected HLA locus is
CC   contacted with the amplified product. This first probe recognises a HLA-
CC   DR beta-allelic polymorphism. A second (different) probe is brought into
CC   contact with a second sample of the amplified DNA in a separate reaction,
CC   and hybridisation detected. The probes and primers are used for HLA
CC   typing, e.g. for tissue, especially bone marrow, transplants
XX
SQ   Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          4 CGGGCCCT 11


RESULT 561
ABH93621/c
ID   ABH93621 standard; DNA; 12 BP.
XX
AC   ABH93621;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 293614 for detecting SNP TSC0015707.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
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```
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 293614; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db         12 TACGTGTA 5


RESULT 562
ABI06748/c
ID   ABI06748 standard; DNA; 12 BP.
XX
AC   ABI06748;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 306721 for detecting SNP TSC0022148.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 306721; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          8 TACGTGTA 1


RESULT 563
ABH95544
ID   ABH95544 standard; DNA; 12 BP.
XX
AC   ABH95544;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 295537 for detecting SNP TSC0016628.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 295537; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          5 CCCTACGT 12
              ||||||||
Db          5 CCCTACGT 12


RESULT 564
ABI56358
ID   ABI56358 standard; DNA; 12 BP.
XX
AC   ABI56358;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 356331 for detecting SNP TSC0050060.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 356331; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          1 TACGTGTA 8


RESULT 565
ABH70251
ID   ABH70251 standard; DNA; 12 BP.
XX
AC   ABH70251;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 270228 for detecting SNP TSC0002052.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 270228; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          2 TACGTGTA 9


RESULT 566
ABH89284
ID   ABH89284 standard; DNA; 12 BP.
XX
AC   ABH89284;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
```

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PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          3 TACGTGTA 10


RESULT 567
ABH92486/c
ID   ABH92486 standard; DNA; 12 BP.
XX
AC   ABH92486;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 292479 for detecting SNP TSC0015230.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 292479; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACG 11
              ||||||||
Db         10 GCCCTACG 3


RESULT 568
ABI13410
ID   ABI13410 standard; DNA; 12 BP.
XX
AC   ABI13410;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 313383 for detecting SNP TSC0025713.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313383; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
```

```
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          5 CCCTACGT 12


RESULT 569
ABI62488
ID   ABI62488 standard; DNA; 12 BP.
XX
AC   ABI62488;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 362461 for detecting SNP TSC0053239.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 362461; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          4 TACGTGTA 11


RESULT 570
ABI13984
ID   ABI13984 standard; DNA; 12 BP.
XX
AC   ABI13984;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 313957 for detecting SNP TSC0026047.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313957; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          2 TACGTGTA 9


RESULT 571
ABH95542/c
ID   ABH95542 standard; DNA; 12 BP.
XX
AC   ABH95542;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 295535 for detecting SNP TSC0016627.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 295535; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCCTACGT 12
||||||||
Db 8 CCCTACGT 1

RESULT 572
ABH76707
ID ABH76707 standard; DNA; 12 BP.
XX
AC ABH76707;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 276700 for detecting SNP TSC0004266.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TACGTGTA 15
||||||||
Db 3 TACGTGTA 10

RESULT 573
ABI76102/c
ID ABI76102 standard; DNA; 12 BP.
XX
AC ABI76102;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 376075 for detecting SNP TSC0061603.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 376075; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

```
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db         10 CCCTACGT 3


RESULT 574
ABH81705
ID   ABH81705 standard; DNA; 12 BP.
XX
AC   ABH81705;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 281698 for detecting SNP TSC0010001.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 281698; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          5 TACGTGTA 12


RESULT 575
ABH85829/c
ID   ABH85829 standard; DNA; 12 BP.
XX
AC   ABH85829;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285822 for detecting SNP TSC0012462.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 285822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db         10 TACGTGTA 3


RESULT 576
ABH86354
ID   ABH86354 standard; DNA; 12 BP.
XX
```

```
AC   ABH86354;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 286347 for detecting SNP TSC0012678.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 286347; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          5 AGGGAGTC 12


RESULT 577
ABI13988
ID   ABI13988 standard; DNA; 12 BP.
XX
AC   ABI13988;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 313961 for detecting SNP TSC0026047.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313961; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          2 TACGTGTA 9


RESULT 578
ABH97060/c
ID   ABH97060 standard; DNA; 12 BP.
XX
AC   ABH97060;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 297053 for detecting SNP TSC0017414.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
```

```
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 297053; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db         10 CCCTACGT 3


RESULT 579
ABI16213
ID   ABI16213 standard; DNA; 12 BP.
XX
AC   ABI16213;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          5 AGGGAGTC 12


RESULT 580
ABI56360
ID   ABI56360 standard; DNA; 12 BP.
XX
AC   ABI56360;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 356333 for detecting SNP TSC0050060.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 356333; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
```

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                ||||||||
Db          1 TACGTGTA 8


RESULT 581
ABI28945/c
ID   ABI28945 standard; DNA; 12 BP.
XX
AC   ABI28945;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 328918 for detecting SNP TSC0034654.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 328918; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db         11 AGGGAGTC 4


RESULT 582
ABI10703/c
ID   ABI10703 standard; DNA; 12 BP.
XX
AC   ABI10703;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db         11 TACGTGTA 4


RESULT 583
ABI75403/c
ID   ABI75403 standard; DNA; 12 BP.
XX
AC   ABI75403;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 375376 for detecting SNP TSC0061224.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
```

```
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 375376; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          9 CCCTACGT 2


RESULT 584
ABI63259
ID   ABI63259 standard; DNA; 12 BP.
XX
AC   ABI63259;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 363232 for detecting SNP TSC0053719.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 363232; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          3 TACGTGTA 10


RESULT 585
ABH73580
ID   ABH73580 standard; DNA; 12 BP.
XX
AC   ABH73580;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
```

```
XX
SQ   Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          3 TACGTGTA 10


RESULT 586
ABI56650/c
ID   ABI56650 standard; DNA; 12 BP.
XX
AC   ABI56650;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 356623 for detecting SNP TSC0050224.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 356623; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db         11 TACGTGTA 4


RESULT 587
ABI59399/c
ID   ABI59399 standard; DNA; 12 BP.
XX
AC   ABI59399;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 359372 for detecting SNP TSC0051583.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 359372; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              ||||||||
Db          9 TACGTGTA 2


RESULT 588
AAF92629
ID   AAF92629 standard; DNA; 12 BP.
XX
AC   AAF92629;
XX
DT   16-MAY-2001  (first entry)
XX
DE   HLA-DR typing probe #9.
XX
KW   Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
KW   ss.
XX
OS   Homo sapiens.
```

XX
PN US6194147-B1.
XX
PD 27-FEB-2001.
XX
PF 30-DEC-1997; 97US-00000805.
XX
PR 27-JUN-1990; 90US-00544218.
PR 08-APR-1993; 93US-00057957.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Baxter-Lowe LA, Gorski JA;
XX
DR WPI; 2001-217923/22.
XX
PT Human leukocyte antigen typing by amplifying a sample followed by
PT sequence specific oligonucleotide hybridization with labeled
PT oligonucleotide probes that hybridize with a series of known control DNA
PT sequences.
XX
PS Disclosure; Col 11-14; 16pp; English.
XX
CC The present invention relates to human leukocyte antigen (HLA) typing.
CC The method involves detecting polymorphic residues by sequence specific
CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
CC probes
XX
SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
||||||||
Db 4 CGGGCCCT 11

RESULT 589
AAF92695
ID AAF92695 standard; DNA; 12 BP.
XX
AC AAF92695;
XX
DT 16-MAY-2001 (first entry)
XX
DE HLA-DR allele group typing probe #10.
XX
KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
KW ss.
XX
OS Homo sapiens.
XX
PN US6194147-B1.
XX
PD 27-FEB-2001.
XX
PF 30-DEC-1997; 97US-00000805.
XX
PR 27-JUN-1990; 90US-00544218.
PR 08-APR-1993; 93US-00057957.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Baxter-Lowe LA, Gorski JA;
XX
DR WPI; 2001-217923/22.
XX
PT Human leukocyte antigen typing by amplifying a sample followed by
PT sequence specific oligonucleotide hybridization with labeled
PT oligonucleotide probes that hybridize with a series of known control DNA
PT sequences.
XX
PS Disclosure; Col 11-14; 16pp; English.
XX
CC The present invention relates to human leukocyte antigen (HLA) typing.
CC The method involves detecting polymorphic residues by sequence specific
CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
CC probes
XX
SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
||||||||
Db 4 CGGGCCCT 11

RESULT 590
ABL42258
ID ABL42258 standard; DNA; 12 BP.
XX
AC ABL42258;
XX
DT 01-JUL-2002 (first entry)
XX
DE Plant cis-regulatory sequence from barley ABA.
XX
KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;
KW gene family; ds.
XX
OS Hordeum sp.
XX
PN WO200162967-A2.
XX
PD 30-AUG-2001.
XX
PF 19-FEB-2001; 2001WO-IL000151.
XX
PR 22-FEB-2000; 2000IL-00134660.
PR 02-JUL-2000; 2000IL-00137124.
PR 20-AUG-2000; 2000IL-00137959.
XX
PA (GENE-) GENENA LTD.
PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
XX
PI Vider B, Katzir N;
XX
DR WPI; 2002-239525/29.
XX
PT Polymerase chain reaction based method of DNA fingerprinting, useful for
PT analyzing genes, e.g. for identifying genes involved in cancer formation,
PT involves using a mix of primers that match the conserved regions of a
PT gene family.
XX
PS Example; Page 17; 28pp; English.
XX
CC The invention relates to a polymerase chain reaction (PCR) based method
CC of DNA fingerprinting, comprising using primers that match the conserved
CC regions of a gene family. The method is useful for gene expression
CC analysis of any cell or tissue, or for the performance of DNA
CC fingerprinting analysis of the same organism in order that one will
CC reveal the function of a gene that produced differential product between
CC genotypes. The method is also useful for identifying PCR reactions that
CC contain a gene of interest in a gene family reverse transcriptase (RT)-
CC PCR expression analysis. The method is also useful for identifying genes
CC that belong to a gene family that might be involved in cancer formation.
CC The method is particularly useful for comparing genomic sequences. These
CC are also applicable in agriculture (e.g. to mark useful genes to assist
CC breeding). The current sequence represents a plant cis-regulatory
CC sequence. This is used in DNA fingerprinting using primers or a mix of
CC primers that match the sequence of ubiquitous cis-acting regulatory

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CC   elements
XX
SQ   Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match            28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTG 13
              ||||||||
Db          1 CCTACGTG 8


RESULT 591
ABX10158
ID   ABX10158 standard; cDNA; 12 BP.
XX
AC   ABX10158;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human TIGR/Myocilin variant cDNA deletion 3' flank #1.
XX
KW   Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness;
KW   trabecular meshwork inducible glucocorticoid responsive protein;
KW   retinal degenerative disease; RDD; retinitis pigmentosa;
KW   macular degeneration; Usher syndrome; cardiovascular disease;
KW   congenital heart disease; myocardial ischaemia; stroke;
KW   acute endocarditis; hypertensive heart disease; arrhythmia;
KW   arteriosclerotic heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200282969-A2.
XX
PD   24-OCT-2002.
XX
PF   11-DEC-2001; 2001WO-US048622.
XX
PR   05-APR-2001; 2001US-0281442P.
PR   23-JUL-2001; 2001US-0306889P.
XX
PA   (KONG/) KONG T H.
XX
PI   Kong TH;
XX
DR   WPI; 2003-058597/05.
XX
PT   Determining the presence or the risk of having glaucoma, retinal
PT   degenerative or cardiovascular diseases in a subject, comprises
PT   generating transcriptional or translational profiles based on myocilin
PT   nucleic acids and proteins.
XX
PS   Disclosure; Fig 4c; 55pp; English.
XX
CC   The invention relates to determining whether a subject has or is at risk
CC   of developing glaucoma, retinal degenerative disease, or a cardiovascular
CC   disease, comprises generating a transcriptional or translational profile
CC   (i.e. 'fingerprint') in the subject or in a sample obtained from the
CC   subject, based on the expression of the different myocilin (MYOC, also
CC   known as trabecular meshwork inducible glucocorticoid responsive protein,
CC   TIGR) mRNA species or polypeptide forms, where a difference in the
CC   profile relative to that in a normal subject indicates that the subject
CC   has or is at risk of developing the above-mentioned diseases. Also
CC   included are: (1) a method for establishing MYOC genetic population
CC   profile in a population of individuals having glaucoma, retinal
CC   degenerative disease, or a cardiovascular disease; (2) a method for
CC   pharmacogenomically selecting a therapy to administer to an individual
CC   having glaucoma, retinal degenerative disease, or a cardiovascular
CC   disease, comprising determining MYOC genetic profile of an individual and
CC   comparing the individual's MYOC genetic profile to MYOC genetic
CC   population profile, to select a therapy for administration to the
CC   individual; and a kit for determining whether a subject has or is likely
CC   to develop glaucoma, retinal degenerative disease, or a cardiovascular
CC   disease, comprising a probe or primer which hybridises to the MYOC
CC   nucleic acid, or an antibody or peptide probe capable of specifically
CC   binding to the novel MYOC polypeptide(s), and instructions for use. The
CC   method is useful for the prognosis and/or diagnosis of glaucoma, retinal
CC   degenerative diseases (RDD) or cardiovascular diseases (e.g. blindness,
CC   retinitis pigmentosa, macular degeneration, Usher syndrome, congenital
CC   heart disease, myocardial ischaemia, stroke, acute endocarditis,
CC   hypertensive heart disease, arrhythmia and arteriosclerotic heart
CC   disease), and in screening assays for the identification of therapeutics
CC   and the evaluation of their effectiveness for treating the above-
CC   mentioned diseases in a subject. The present sequence represents the 3'
CC   flanking sequence surrounding the deletion present in a MYOC cDNA variant
XX
SQ   Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match            28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db          2 GAGTCCAG 9


RESULT 592
AAX09580/c
ID   AAX09580 standard; DNA; 15 BP.
XX
AC   AAX09580;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic marker upstream primer #460.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US020313.
XX
PR   06-NOV-1996;   96US-0030455P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Lander ES,  Wang D,  Hudson T;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease.
XX
PS   Claim 15; Page 207; 310pp; English.
XX
CC   AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC   isolation of various biallelic polymorphic markers found in the human
CC   genome (represented in AAX10269-X12937). These primers can be used in a
CC   method for determining polymorphic forms in an individual for use in e.g.
CC   forensics, paternity testing or for phenotypic typing for diseases such
CC   as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC   hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
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CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases
XX
SQ   Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAG 22
              ||||||||
Db         14 ACAGGGAG 7


RESULT 593
ABV65206
ID   ABV65206 standard; cDNA; 11 BP.
XX
AC   ABV65206;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2992.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 108; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 3e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | ||||||
Db          1 CTTCCTGTACA 11


RESULT 594
ABK99385/c
ID   ABK99385 standard; DNA; 11 BP.
XX
AC   ABK99385;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human CYP3A5 gene polymorphic reference DNA sequence #20.
XX
KW   Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW   AIDS; African American; forensic marker; pharmacological; cytostatic;
KW   antidiabetic; anti-HIV; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200253775-A2.
XX
PD   11-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-EP015290.
XX
PR   28-DEC-2000; 2000EP-00128627.
PR   28-DEC-2000; 2000US-0258684P.
PR   29-DEC-2000; 2000US-0258952P.
PR   16-JAN-2001; 2001EP-00100172.
PR   18-JAN-2001; 2001US-0262859P.
PR   16-AUG-2001; 2001EP-00118884.
PR   16-AUG-2001; 2001US-0312825P.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Wojnowski L,  Haberl M,  Hustert E;
XX
DR   WPI; 2002-583628/62.
XX
PT   Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT   cardiovascular diseases, diabetes and AIDS, and for identifying
PT   polymorphisms.
XX
PS   Example 2; Page 49; 138pp; English.
XX
CC   The present invention relates to a new CYP3A5 polynucleotide encoding a
CC   polypeptide, where the polynucleotide is capable of hybridising to a
CC   CYP3A5 gene. The invention is useful in an in vitro method for
CC   identifying a polymorphism. The invention is also useful for useful for
CC   diagnosing a disorder related to the presence of a molecular variant of a
CC   CYP3A5 or susceptibility to such a disorder, where the disorder is
CC   cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC   The invention can further be used for the preparation of a diagnostic
CC   composition for diagnosing a disease in a subject having a genome
CC   comprising a variant allele of the CYP3A5 gene, where the subject is an
CC   African American. The molecules of the invention are as forensic markers
CC   and in pharmacological studies. The present nucleic acid sequence
CC   represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC   described in the invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 3e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||| | |||||
Db         11 CCTTCCTGTAC 1
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RESULT 595
ABI23374/c
ID   ABI23374 standard; DNA; 12 BP.
XX
AC   ABI23374;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 323347 for detecting SNP TSC0031342.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 323347; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 3.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              |||||| |||
Db         11 CCCTACACGTA 1


RESULT 596
ABI18399/c
ID   ABI18399 standard; DNA; 12 BP.
XX
AC   ABI18399;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 318372 for detecting SNP TSC0028620.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 318372; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 3.4e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||| ||| ||
Db          12 TGTAGAGGTAG 2


RESULT 597
ABF18031/c
ID   ABF18031 standard; DNA; 13 BP.
XX
AC   ABF18031;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118028 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
```

```
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118028; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   81.8%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| ||| ||
Db         13 TGTAGAGGTAG 3


RESULT 598
ABF18030
ID   ABF18030 standard; DNA; 13 BP.
XX
AC   ABF18030;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118027 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118027; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   81.8%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| ||| ||
Db          1 TGTAGAGGTAG 11


RESULT 599
ABF19283/c
ID   ABF19283 standard; DNA; 13 BP.
XX
AC   ABF19283;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 119280 for detecting SNP TSC0029787.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 119280; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;
```

```
  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   69.2%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              |||| | | |||:
Db         13 TGTAAACGTAGTY 1


RESULT 600
ABF44695/c
ID   ABF44695 standard; DNA; 13 BP.
XX
AC   ABF44695;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 144692 for detecting SNP TSC0036396.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 144692; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   69.2%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              |||| | | |||:
Db         13 TGTAGACGTAGTY 1


RESULT 601
ABF19282
ID   ABF19282 standard; DNA; 13 BP.
XX
AC   ABF19282;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 119279 for detecting SNP TSC0029787.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 119279; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   69.2%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              |||| | | |||:
Db          1 TGTAAACGTAGTY 13


RESULT 602
ABF44694
ID   ABF44694 standard; DNA; 13 BP.
XX
AC   ABF44694;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 144691 for detecting SNP TSC0036396.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
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```
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 144691; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   69.2%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              |||| | | |||:
Db          1 TGTAGACGTAGTY 13


RESULT 603
ABF36730/c
ID   ABF36730 standard; DNA; 13 BP.
XX
AC   ABF36730;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136727 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136727; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   81.8%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || ||| ||||
Db         11 CTCCGTTTACA 1


RESULT 604
ABF36731
ID   ABF36731 standard; DNA; 13 BP.
XX
AC   ABF36731;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136728 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136728; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
```

```
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 13;
  Best Local Similarity   81.8%;  Pred. No. 3.8e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || ||| ||||
Db          3 CTCCGTTTACA 13


RESULT 605
ADB01855/c
ID   ADB01855 standard; DNA; 25 BP.
XX
AC   ADB01855;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2841.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2841; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 5.3e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         23 GCACTCGCTGCACACGTAG 5


RESULT 606
ADB01856/c
ID   ADB01856 standard; DNA; 25 BP.
XX
AC   ADB01856;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2842.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2842; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 5.3e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         22 GCACTCGCTGCACACGTAG 4
```

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RESULT 607
ADB01854/c
ID   ADB01854 standard; DNA; 25 BP.
XX
AC   ADB01854;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2840.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2840; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 5.3e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         24 GCACTCGCTGCACACGTAG 6


RESULT 608
ADB01853/c
ID   ADB01853 standard; DNA; 25 BP.
XX
AC   ADB01853;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2839.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2839; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 5.3e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         25 GCACTCGCTGCACACGTAG 7


RESULT 609
ADB01857/c
ID   ADB01857 standard; DNA; 25 BP.
XX
AC   ADB01857;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2843.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
```

XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 2843; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 5.3e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GCCCTACGTGTACAGGGAG 22
|| || || ||| | ||
Db 21 GCACTCGCTGCACACGTAG 3

RESULT 610
ADB01858/c
ID ADB01858 standard; DNA; 25 BP.
XX
AC ADB01858;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 2844.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 2844; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 5 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;
Best Local Similarity 63.2%; Pred. No. 5.3e+02;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GCCCTACGTGTACAGGGAG 22
|| || || ||| | ||
Db 20 GCACTCGCTGCACACGTAG 2

RESULT 611
AAF47954
ID AAF47954 standard; DNA; 15 BP.
XX
AC AAF47954;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1374.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.

```
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 8 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 4.8e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAG 18
              | ||  |  ||||||
Db          2 CACTCCCCGTACAG 15


RESULT 612
AAF47955
ID   AAF47955 standard; DNA; 15 BP.
XX
AC   AAF47955;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1375.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 4.8e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAG 18
              | ||  |  ||||||
Db          1 CACTCCCCGTACAG 14


RESULT 613
AAF47956
ID   AAF47956 standard; DNA; 15 BP.
XX
AC   AAF47956;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1376.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
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PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 4.8e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGG 20
              || |  ||||| |
Db          2 CTCCCCGTACAGTG 15


RESULT 614
ABA80105/c
ID   ABA80105 standard; DNA; 17 BP.
XX
AC   ABA80105;
XX
DT   24-JAN-2002  (first entry)
XX
DE   HBA2 mutation correcting oligonucleotide SEQ ID NO: 2951.
XX
KW   Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW   retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW   cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW   adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW   haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW   mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW   familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW   UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW   Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW   antilipemic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173002-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009761.
XX
PR   27-MAR-2000; 2000US-0192176P.
PR   27-MAR-2000; 2000US-0192179P.
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC;
XX
DR   WPI; 2001-639230/73.
XX
PT   Oligonucleotide for targeted alterations of genetic sequences and for
PT   treating cystic fibrosis, comprises at least one mismatch and chemical
PT   modification.
XX
PS   Claim 7; Page 208; 294pp; English.
XX
CC   The present invention provides single-stranded oligonucleotides which can
CC   be used for the targeted alteration of genomic sequences, where the
CC   oligonucleotide has at least one mismatch compared with the genomic
CC   sequence to be altered. In particular, these sequences are directed at
CC   the following genes: adenosine deaminase, p53, beta-globin,
CC   retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC   (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC   1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC   apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC   (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC   presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC   such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC   haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC   Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC   various syndromes. The present sequence is one of the gene correcting
CC   oligonucleotides of the invention
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 5.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              ||| | || ||| |
Db         15 CCTCCCTGGACAAG 2


RESULT 615
ABA80104
ID   ABA80104 standard; DNA; 17 BP.
XX
AC   ABA80104;
XX
DT   24-JAN-2002  (first entry)
XX
DE   HBA2 mutation correcting oligonucleotide SEQ ID NO: 2950.
XX
KW   Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW   retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW   cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW   adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW   haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW   mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW   familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW   UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW   Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW   antilipemic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173002-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009761.
XX
PR   27-MAR-2000; 2000US-0192176P.
PR   27-MAR-2000; 2000US-0192179P.
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC;
XX
DR   WPI; 2001-639230/73.
XX
PT   Oligonucleotide for targeted alterations of genetic sequences and for
```

```
PT   treating cystic fibrosis, comprises at least one mismatch and chemical
PT   modification.
XX
PS   Claim 7; Page 208; 294pp; English.
XX
CC   The present invention provides single-stranded oligonucleotides which can
CC   be used for the targeted alteration of genomic sequences, where the
CC   oligonucleotide has at least one mismatch compared with the genomic
CC   sequence to be altered. In particular, these sequences are directed at
CC   the following genes: adenosine deaminase, p53, beta-globin,
CC   retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC   (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC   1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC   apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC   (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC   presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC   such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC   haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC   Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC   various syndromes. The present sequence is one of the gene correcting
CC   oligonucleotides of the invention
XX
SQ   Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 5.2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              ||| | || ||| |
Db          3 CCTCCCTGGACAAG 16


RESULT 616
ADD71263
ID   ADD71263 standard; DNA; 10 BP.
XX
AC   ADD71263;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Mouse ET gene 5' splice donor site from intron 4.
XX
KW   Mouse; ethenolaminephosphate cytidilyl transferase; ET; ds;
KW   splice donor site; antilipemic; cardiant; anorectic;
KW   phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
KW   cardiovascular disease; atherosclerosis; obesity.
XX
OS   Mus musculus.
XX
PN   US2003194795-A1.
XX
PD   16-OCT-2003.
XX
PF   21-MAR-2002; 2002US-00101957.
XX
PR   21-MAR-2002; 2002US-00101957.
XX
PA   (BAKO/) BAKOVIC M.
PA   (POLO/) POLOUMIENKO A.
XX
PI   Bakovic M,  Poloumienko A;
XX
DR   WPI; 2003-844457/78.
XX
PT   New gene encoding a protein having ethanolaminephosphate
PT   cytidyltransferase activity, useful for treating Zellweger's syndrome, or
PT   lipid-related diseases such as cardiovascular diseases and obesity.
XX
PS   Example 1; Page 6; 22pp; English.
XX
CC   The invention relates to a mouse gene encoding a protein having
CC   ethanolaminephosphate cytidyltransferase (ET) activity appearing as
CC   ADD71226, a degenerate variant of the ET gene, or a sequence that
CC   hybridises to the complement of the ET gene under stringent conditions.
CC   Also included is a promoter of a human ethanolaminephosphate
CC   cytidyltransferase gene appearing as ADD71227. The gene and promoter are
CC   useful for producing a transgenic animal, and for identifying,
CC   preventing, and treating diseases (by gene therapy) related to
CC   inappropriate phosphatidylethanolamine production, e.g. Zellweger's
CC   syndrome, or lipid-related diseases such as cardiovascular diseases,
CC   atherosclerosis and obesity. The present sequence is a mouse ET gene 5'
CC   splice donor site.
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             26.4%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 3.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAG 22
              |||||| ||
Db          1 TACAGGTAG 9


RESULT 617
AAZ83886/c
ID   AAZ83886 standard; DNA; 10 BP.
XX
AC   AAZ83886;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3120.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 142; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
```

```
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             26.4%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 3.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACA 17
              || ||||||
Db         10 ACCTGTACA 2


RESULT 618
AAF37857
ID   AAF37857 standard; DNA; 10 BP.
XX
AC   AAF37857;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4596.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 164; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             26.4%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 3.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGG 19
              ||||||| |
Db          2 GTGTACACG 10


RESULT 619
ABH73586
ID   ABH73586 standard; DNA; 12 BP.
XX
AC   ABH73586;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273571 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273571; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
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CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             26.4%;  Score 7.4;  DB 1;  Length 12;
  Best Local Similarity   88.9%;  Pred. No. 4.1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||| ||||
Db          3 TACGCGTAC 11


RESULT 620
AAQ87648
ID   AAQ87648 standard; DNA; 18 BP.
XX
AC   AAQ87648;
XX
DT   19-DEC-1995  (first entry)
XX
DE   Chick antisense oligonucleotide to p75 NGFR gene.
XX
KW   Oligonucleotide; antisense; down-regulation; expression; trauma;
KW   nerve growth factor receptor; neurodegenerative disease; Alzheimer's;
KW   Parkinson's; Hungtington's disease; multiple sclerosis;
KW   vascular ischaemia; stroke; ss.
XX
OS   Synthetic.
XX
PN   WO9511253-A1.
XX
PD   27-APR-1995.
XX
PF   18-OCT-1994;   94WO-AU000631.
XX
PR   18-OCT-1993;   93AU-00001870.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Barrett GL;
XX
DR   WPI; 1995-170186/22.
XX
PT   Anti:sense oligo:nucleotide(s) to nerve growth factor receptor gene - of
PT   p75 NGFR, down-regulate expression and enhance neurone survival; for
PT   treating cerebal palsy, Alzheimer's disease, stroke, etc.
XX
PS   Example 3; Page 35; 59pp; English.
XX
CC   The sequence of an antisense oligonucleotide to the chick nerve growth
CC   factor receptor (NGFR) gene which was used as a control for the survival
CC   of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides
CC   AAQ87641-2. These oligonucleotides are antisense sequences directed at
CC   down-regulating the expression of the gene encoding the mouse p75 NGFR
CC   gene. The oligonucleotides can be used in methods to treat
CC   neurodegenerative conditions associated with disease and/or trauma such
CC   as Alzheimer's, Parkinson's or Hungtington's disease, multiple sclerosis,
CC   vascular ischaemia associated with stroke, etc
XX
SQ   Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             26.4%;  Score 7.4;  DB 1;  Length 18;
  Best Local Similarity   64.7%;  Pred. No. 5.8e+02;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCCAG 27
              ||| ||   |  || |||
Db          2 GTGGACTCGCTGTACAG 18


RESULT 621
```

```
ABI23376
ID   ABI23376 standard; DNA; 12 BP.
XX
AC   ABI23376;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 323349 for detecting SNP TSC0031342.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 323349; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||| |||  ||
Db          1 TACGCGTAGGGG 12


RESULT 622
ABH73584/c
ID   ABH73584 standard; DNA; 12 BP.
XX
AC   ABH73584;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273569 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273569; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | |||  |||||
Db         12 CGTACACGTACA 1


RESULT 623
AAZ41746
ID   AAZ41746 standard; DNA; 12 BP.
XX
AC   AAZ41746;
XX
DT   20-MAR-2003  (revised)
DT   21-JAN-2000  (first entry)
XX
DE   Organic material detecting primer 107.
XX
KW   Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW   detection; pollutant; soil; food; agricultural chemical; polymer;
KW   organochlorine; primer; ss.
XX
OS   Synthetic.
XX
PN   DE19914461-A1.
XX
PD   21-OCT-1999.
XX
PF   30-MAR-1999;   99DE-01014461.
XX
PR   31-MAR-1998;   98JP-00087651.
PR   16-MAR-1999;   99JP-00069694.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI   Inoue T;
XX
DR   WPI; 1999-592157/51.
XX
PT   Novel polymerase chain reaction method, for differentiating between
PT   microorganisms and for detecting contaminants.
XX
PS   Example 1; Page 19; 78pp; German.
XX
CC   This invention describes a novel method for the amplification of DNA
CC   comprising (i) preparing many primers (P) with different probabilities of
CC   amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC   many different DNA using these primers. The method is used (i) to
CC   differentiate between different microorganisms in a mixed population and
CC   (ii) to determine presence/absence of an impurity (pollutant), or its
CC   concentration, in e.g. soil, foods, compost etc., typically metals,
CC   agricultural chemicals, polymers, organochlorine compounds etc. A
CC   particular use is monitoring composting of organic material.
CC   Amplification with many primers produces a lot of information, so
CC   reliability of the test is improved, and many samples may be tested
CC   quickly. AAZ41640-Z41855 represent the primers described in the method of
CC   the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              | |||||  | ||
Db          1 GAGTACACGAAG 12


RESULT 624
AAZ41530
ID   AAZ41530 standard; DNA; 12 BP.
XX
AC   AAZ41530;
XX
DT   19-JAN-2000  (first entry)
XX
DE   Microbe detection in organic waste arbitrarily primed PCR primer #107.
XX
KW   Microbe; detection; organic waste; arbitrarily primer PCR;
KW   random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP11276176-A.
XX
PD   12-OCT-1999.
XX
PF   31-MAR-1998;   98JP-00087652.
XX
PR   31-MAR-1998;   98JP-00087652.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 1999-626940/54.
XX
PT   Amplification of a DNA fragment - in order to establish the state of
PT   existence of a microbe.
XX
PS   Claim 1; Page 9; 40pp; Japanese.
XX
CC   A method has been developed for the amplification of a DNA fragment in
CC   which amplification is carried out on the DNA fragments of a number of
CC   different DNAs. The method comprises a PCR reaction repeatedly carrying
CC   out a heat-denaturing step, a primer annealing step and a polymerase
```

```
CC   extending step, to amplify the DNA fragments of a plural of different
CC   DNAs. The method can detect the existence of a microbe in organic waste.
CC   AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC   polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC   organic waste
XX
SQ   Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              | ||||| | ||
Db          1 GAGTACACGAAG 12


RESULT 625
AAC97881
ID   AAC97881 standard; DNA; 12 BP.
XX
AC   AAC97881;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Primer used to illustrate DNA amplification method SEQ ID 107.
XX
KW   Primer; amplification; selective; ss.
XX
OS   Synthetic.
XX
PN   JP2000270867-A.
XX
PD   03-OCT-2000.
XX
PF   19-MAR-1999;   99JP-00076844.
XX
PR   19-MAR-1999;   99JP-00076844.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 2001-011047/02.
XX
PT   Amplification of a DNA fragment and its apparatus.
XX
PS   Example 1; Page 9; 32pp; Japanese.
XX
CC   This invention relates to a method for amplifying a DNA fragment. The
CC   method comprises successive repetitions of heat-denaturing, annealing of
CC   a primer and an extending step using a DNA polymerase. The method makes
CC   use of a cDNA pool in which the primer is one primer or a pair of primer
CC   sets and has an amplification probability which allows it to amplify a
CC   DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC   the limited number is in the range of 1 to 25). Also included in the
CC   invention are apparatus used for carrying out the method, a primer and a
CC   DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC   can be used to amplify a limited number of cDNAs from a pool in which a
CC   wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC   represent primers used in an example illustrating the method of the
CC   invention
XX
SQ   Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              | ||||| | ||
Db          1 GAGTACACGAAG 12


RESULT 626
ABH73580/c
ID   ABH73580 standard; DNA; 12 BP.
XX
AC   ABH73580;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | |||  |||||
Db         12 CATACACGTACA 1


RESULT 627
ABH30582/c
ID   ABH30582 standard; DNA; 13 BP.
XX
AC   ABH30582;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 230559 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              ||| |||| | |
Db         13 CGTATACACGTA 2


RESULT 628
ABC62971
ID   ABC62971 standard; DNA; 13 BP.
XX
AC   ABC62971;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62988; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||| | |||| |
Db          2 TACCTTTACACG 13


RESULT 629
ABC62970/c
ID   ABC62970 standard; DNA; 13 BP.
XX
AC   ABC62970;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62987 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
```

```
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||| | ||||  |
Db         12 TACCTTTACACG 1


RESULT 630
ABC62969
ID   ABC62969 standard; DNA; 13 BP.
XX
AC   ABC62969;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62986 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62986; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||| | ||||  |
Db          2 TACCTCTACACG 13


RESULT 631
ABC62968/c
ID   ABC62968 standard; DNA; 13 BP.
XX
AC   ABC62968;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62985 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||| | ||||  |
Db         12 TACCTCTACACG 1


RESULT 632
ABH30583
ID   ABH30583 standard; DNA; 13 BP.
XX
AC   ABH30583;
```

```
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 230560 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230560; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 5e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
               ||| |||| | |
Db          1 CGTATACACGTA 12


RESULT 633
AAA52434
ID   AAA52434 standard; DNA; 15 BP.
XX
AC   AAA52434;
XX
DT   18-SEP-2000  (first entry)
XX
DE   TdT-expressing Ramos cell VH insertion+deletion mutation, F264.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB003358.
XX
PR   09-OCT-1998;   98GB-00022104.
PR   19-JAN-1999;   99GB-00001141.
PR   09-JUN-1999;   99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE,  Neuberger MS,  Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 4; Fig 6; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
CC   an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. This was determined on the
CC   basis of the amount of diversity in the heavy chain variable region (VH).
CC   Sequences AAA52366-A52434 represent fragments of Ramos cell VH region DNA
CC   containing mutations other than single nucleotide substitutions. The
CC   number assigned to the mutation represents the position in the wild-type
CC   VH DNA (AAA52364) to which the first nucleotide in the mutant fragment
CC   corresponds. Sequences AAA52388-A52434 represent mutations that occur in
CC   Ramos cells which express TdT, and sequences AAA52366-A52487 represent
CC   mutations that occur in non-TdT- expressing control Ramos cells
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 15;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
               ||| ||| || |
Db          3 GTGCACATGGGG 14


RESULT 634
AAZ62686/c
ID   AAZ62686 standard; RNA; 15 BP.
XX
AC   AAZ62686;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV-5596 which cleaves HCV RNA at nt. 5596.
XX
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KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 59; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 15;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAGTCCA 26
               ||  ||| ||||
Db          13 ACCTGGACTCCA 2


RESULT 635
ABX00537/c
ID   ABX00537 standard; RNA; 15 BP.
XX
AC   ABX00537;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #319 for HCV hammerhead ribozyme #319.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 30; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

  Query Match             25.7%;  Score 7.2;  DB 1;  Length 15;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAGTCCA 26
               ||  ||| ||||
Db          13 ACCTGGACTCCA 2


RESULT 636
AAF43233
ID   AAF43233 standard; DNA; 10 BP.
XX
AC   AAF43233;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11372.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
```

XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 356; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
|||||||
Db 2 GGAGTCC 8

RESULT 637
AAF36719
ID AAF36719 standard; DNA; 10 BP.
XX
AC AAF36719;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3458.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX

PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 123; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCCT 8
|||||||
Db 3 GGGCCCT 9

RESULT 638
ABQ86579/c
ID ABQ86579 standard; cDNA; 11 BP.
XX
AC ABQ86579;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 334.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX

PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 50; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
|||||||
Db 9 GGAGTCC 3

RESULT 639
ABV64991/c
ID ABV64991 standard; cDNA; 11 BP.
XX
AC ABV64991;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2777.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 102; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
|||||||
Db 9 GGAGTCC 3

RESULT 640
AAZ90850
ID AAZ90850 standard; DNA; 15 BP.
XX
AC AAZ90850;
XX
DT 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #78.
XX
KW Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
OS Homo sapiens.
XX
PN WO9967290-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-JP003351.
XX
PR 24-JUN-1998; 98JP-00214720.
PR 19-OCT-1998; 98JP-00297409.
XX
PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
DR WPI; 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
PS Example 1; Page 41; 176pp; Japanese.
XX
CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC were initially searched for comparison on a nucleic acid database with
CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC Z90925 represent specific examples of probe sequences used in the search.
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC formation disorders. Compounds identified as binding to the proteins are

```
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             25.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCC 25
              |||||||
Db          2 GGAGTCC 8


RESULT 641
AAZ90834
ID   AAZ90834 standard; DNA; 15 BP.
XX
AC   AAZ90834;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #62.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             25.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCC 25
              |||||||
Db          2 GGAGTCC 8


RESULT 642
AAZ90885
ID   AAZ90885 standard; DNA; 15 BP.
XX
AC   AAZ90885;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #113.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             25.0%;  Score 7;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCC 25
              |||||||
Db          2 GGAGTCC 8


RESULT 643
AAZ90922
ID   AAZ90922 standard; DNA; 15 BP.
XX
AC   AAZ90922;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #150.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
```

PR 24-JUN-1998; 98JP-00214720.
PR 19-OCT-1998; 98JP-00297409.
XX
PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
DR WPI; 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
PS Example 1; Page 45; 176pp; Japanese.
XX
CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC were initially searched for comparison on a nucleic acid database with
CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC Z90925 represent specific examples of probe sequences used in the search.
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC formation disorders. Compounds identified as binding to the proteins are
CC used for the treatment of such disorders
XX
SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
|||||||
Db 2 GGAGTCC 8

RESULT 644
ABL46308/c
ID ABL46308 standard; DNA; 17 BP.
XX
AC ABL46308;
XX
DT 26-APR-2002 (first entry)
XX
DE Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:275.
XX
KW Nucleic acid accessible hybridisation site; detection; hybridisation;
KW characterisation; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Claim 48; Fig 79A; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 11 GTGTACAGGGAGTCC 25
|| ||| | ||||
Db 15 GTAGACATAGGGTCC 1

RESULT 645
AAA11710/c
ID AAA11710 standard; DNA; 19 BP.
XX
AC AAA11710;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human prostate-specific antigen PCR primer #4.
XX
KW Prostate-specific antigen; PSA; detection; prostate cancer; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN JP2000069969-A.
XX
PD 07-MAR-2000.
XX
PF 28-AUG-1998; 98JP-00243419.
XX
PR 28-AUG-1998; 98JP-00243419.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (NIID-) NIPPON IDENSHI KENKYUSHO KK.
XX
DR WPI; 2000-264446/23.
XX
PT A primer DNA and detection of an mRNA encoding a prostate-specific
PT antigen by using it.
XX
PS Claim 2; Page 9; 10pp; Japanese.
XX
CC This invention describes novel primers used in a method of detecting an
CC mRNA encoding prostate-specific antigen (PSA) in which cDNA synthesis is
CC carried out by using an mRNA encoding PSA contained in a sample as the
CC first template and then carrying out PCR using one of four described
CC primers to generate a second template. A further a PCR is carried out to
CC generate a third template. The primer DNA is used for the specific
CC detection of prostate cancer. The method is sensitive and specific.
CC AAA11707-A11710 represent the PCR primers described in the method of the
CC invention
XX
SQ Sequence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          8 TACGTGTACAGGGAG 22
              | | ||||||   ||
Db         19 TCCCTGTACACCAAG 5
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RESULT 646
AAF38150
ID   AAF38150 standard; DNA; 10 BP.
XX
AC   AAF38150;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4889.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 174; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match           24.3%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 4.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              | | ||||||
Db          1 TCCCTGTACA 10
```

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RESULT 647
AAF40202
ID   AAF40202 standard; DNA; 10 BP.
XX
AC   AAF40202;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 247; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
```

```
SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 4.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCA 26
              | ||| ||||
Db          1 ATGGACTCCA 10


RESULT 648
ABQ86347
ID   ABQ86347 standard; cDNA; 11 BP.
XX
AC   ABQ86347;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 102.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 41; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              | | ||||||
Db          1 TCCCTGTACA 10


RESULT 649
ABV68461
ID   ABV68461 standard; cDNA; 11 BP.
XX
AC   ABV68461;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6247.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 198; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              | | ||||||
Db          1 TCCCTGTACA 10


RESULT 650
ABH89284/c
ID   ABH89284 standard; DNA; 12 BP.
XX
AC   ABH89284;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
```

```
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||||| |||
Db         12 CCTACACGTA 3


RESULT 651
ABH76707/c
ID   ABH76707 standard; DNA; 12 BP.
XX
AC   ABH76707;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 276700 for detecting SNP TSC0004266.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              ||| |||||
Db         10 TACACGTACA 1


RESULT 652
ABH85829
ID   ABH85829 standard; DNA; 12 BP.
XX
AC   ABH85829;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285822 for detecting SNP TSC0012462.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 285822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
```

```
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              |||  |||||
Db          3 TACACGTACA 12


RESULT 653
ABI10703
ID   ABI10703 standard; DNA; 12 BP.
XX
AC   ABI10703;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 12;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              |||||  |||
Db          2 CCTACACGTA 11


RESULT 654
AAV11115/c
ID   AAV11115 standard; RNA; 13 BP.
XX
AC   AAV11115;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DRB 19DRB #5.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 4 A; 3 C; 5 G; 0 T; 1 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 13;
  Best Local Similarity   80.0%;  Pred. No. 5.9e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              | |||| |||
```

```
Db         12 CCGGGATTCC 3


RESULT 655
ABC09239
ID   ABC09239 standard; DNA; 13 BP.
XX
AC   ABC09239;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 9230 for detecting SNP TSC0002450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 9230; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 13;
  Best Local Similarity   80.0%;  Pred. No. 5.9e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              |||  |||||
Db          2 TACACGTACA 11


RESULT 656
ABC09238/c
ID   ABC09238 standard; DNA; 13 BP.
XX
AC   ABC09238;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 9229 for detecting SNP TSC0002450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 9229; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 13;
  Best Local Similarity   80.0%;  Pred. No. 5.9e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              |||  |||||
Db          2 TACACGTACA 11


RESULT 657
AAA26121/c
ID   AAA26121 standard; DNA; 14 BP.
XX
AC   AAA26121;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2619.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
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```
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 79; Page 98; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 14 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 14;
  Best Local Similarity   80.0%;  Pred. No. 6.2e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               ||||| || |
Db          14 GTACACGGCG 5


RESULT 658
AAQ83430
ID   AAQ83430 standard; DNA; 14 BP.
XX
AC   AAQ83430;
XX
DT   25-MAR-2003  (revised)
DT   20-SEP-1995  (first entry)
XX
DE   c-fos antisense oligonucleotide.
XX
KW   c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW   phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO9502051-A2.
XX
PD   19-JAN-1995.
XX
PF   06-JUL-1994;   94WO-EP002218.
XX
PR   10-JUL-1993;   93EP-00111059.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen G,  Schlingensiepen R,  Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1995-066896/09.
XX
PT   Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT   treating neuronal injury, degeneration, cell death and/or neoplasms.
XX
PS   Claim 2; Page 65; 86pp; English.
XX
CC   Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
CC   comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC   causal role in neuronal injury, degeneration, cell death and/ or
CC   neoplasms, can be used to prevent and treat such conditions. c-jun
CC   antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC   antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC   fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC   Preferably the antisense sequences are phosphorothioate oligonucleotides
CC   since these are not destroyed as fast by endogenous factors as naturally
CC   occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 14;
  Best Local Similarity   80.0%;  Pred. No. 6.2e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGG 20
               || ||||| |
Db           4 GTATACAGAG 13


RESULT 659
ABL39464/c
ID   ABL39464 standard; DNA; 15 BP.
XX
AC   ABL39464;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human ETFB allele-specific oligonucleotide primer 24.
XX
KW   Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW   electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW   novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW   ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW   primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200202580-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021306.
XX
PR   05-JUL-2000; 2000US-0215984P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Bieglecki KM,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-154722/20.
XX
PT   Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT   useful for therapeutic purposes, for studying the expression and function
PT   of the polynucleotide, and for expressing the flavoprotein.
XX
PS   Claim 17; Page 14; 143pp; English.
XX
CC   The invention comprises DNA, cDNA and protein sequences of the human
CC   electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC   chromosome 19q13.3-13.4). The invention specifically relates to the
```

```
CC   identification of 27 novel polymorphic sites within the ETFB gene.
CC   Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC   for nine primary flavoprotein dehydrogenases and is located in the
CC   mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC   (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC   mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC   Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC   Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC   GAII. The novel ETFB polymorphisms identified in the invention are useful
CC   for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC   protein and nucleic acids of the invention are useful for studying the
CC   expression and function of ETFB in vivo. The ETFB protein and nucleic
CC   acids are also useful for testing the efficacy of therapeutic agents and
CC   compounds for glutaric acidaemia type II. The nucleic acids of the
CC   invention are useful in the production of a transgenic animal expressing
CC   the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC   allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC   ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC   represent claimed ETFB primer-extension oligonucleotides
XX
SQ   Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||| ||| ||
Db         10 GGACTCCTGG 1


RESULT 660
ABA03963
ID   ABA03963 standard; DNA; 15 BP.
XX
AC   ABA03963;
XX
DT   19-FEB-2002  (first entry)
XX
DE   Human STK11 gene polymorphism detection ASO primer SEQ ID NO:30.
XX
KW   Human; STK11; serine/threonine kinase 11; polymorphism; SNP;
KW   single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;
KW   haplotype; genetic variant; haplotyping; allele-specific oligonucleotide;
KW   ASO; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200187906-A2.
XX
PD   22-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016045.
XX
PR   17-MAY-2000; 2000US-0204697P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Chew A,  Choi JY,  Nandabalan K,  Sausker EA;
XX
DR   WPI; 2002-055679/07.
XX
PT   Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers
PT   syndrome) useful in studying expression and function of the protein, and
PT   for screening candidate drugs to treat diseases e.g. Peutz-Jeghers
PT   syndrome.
XX
PS   Claim 16; Page 13; 86pp; English.
XX
CC   The present invention describes a method for haplotyping the
CC   serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an
CC   individual. STK11 gene sequences can be used in gene therapy. The STK11
CC   gene is useful for screening drug targeting comprising contacting STK11
CC   with a candidate agent and assaying for binding activity. STK11 is useful
CC   for improving the efficiency and reliability of several steps in the
CC   discovery and development of drugs for treating diseases associated with
CC   STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for
CC   haplotyping the STK11 gene in an individual, which can also be used in
CC   pharmaceutical research to validate STK11 as a candidate target for, and
CC   in design of clinical trials of candidate drugs for, treating a specific
CC   condition drugs or disease predicted to be associated with STK11
CC   activity. Allele-specific oligonucleotides (ASOs) are useful as probes
CC   and primers for assaying a polymorphism in the target region. The present
CC   sequence represents an ASO primer used for detecting STK11 gene
CC   polymorphisms, which is used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 BP; 2 A; 6 C; 6 G; 0 T; 0 U; 1 Other;

  Query Match             24.3%;  Score 6.8;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 6.4e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              || |||| ||
Db          1 CACGGAGGCC 10


RESULT 661
AAA51767/c
ID   AAA51767 standard; DNA; 16 BP.
XX
AC   AAA51767;
XX
DT   31-OCT-2000  (first entry)
XX
DE   CYP3A5 gene 5' flanking region forward sequencing primer 3A5p01.
XX
KW   CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;
KW   Activator protein-3 motif; AP-3; basic transcription element;
KW   drug metabolism; phenotype; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039332-A1.
XX
PD   06-JUL-2000.
XX
PF   22-DEC-1999;   99WO-GB004380.
XX
PR   23-DEC-1998;   98GB-00028619.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Paulussen ADC,  Armstrong M;
XX
DR   WPI; 2000-452418/39.
XX
PT   Identifying subjects with a high drug metabolizing phenotype associated
PT   with cytochrome CYP3A5 expression for establishing whether a drug will be
PT   metabolized by the subject.
XX
PS   Disclosure; Page 39; 68pp; English.
XX
CC   Cytochrome P450 subfamily CYP3A5 transcription regulatory regions can be
CC   screened for the presence/absence of a polymorphic variant, preferably at
CC   positions -475 or -147 of the DNA of the 5' flanking region adjacent to
CC   the CYP3A5 coding sequence. The variants are present in an activator
CC   protein-3 (AP-3) motif and/or a basic transcription element (BTE). The
CC   polymorphisms cause increased CYP3A5 gene expression and this has been
CC   linked to drug metabolic activity. Screening for the presence of variants
CC   can be used to identify subjects with a high or low drug metabolizing
CC   phenotype associated with cytochrome CYP3A5 expression. Primers are used
CC   which in addition to hybridizing to the site of interest, are capable of
CC   introducing a restriction site which is absent in either the wild type
CC   sequence or polymorphic variants. Restriction enzyme cleavage analysis
```

CC can then be used to indicate the presence or absence of the variant. The
CC methods are used to establish, before treatment with a drug, whether the
CC drug will be effectively metabolized by the patient, to identify
CC compounds and transcription factors that can bind to a DNA sequence
CC encoding CYP3A5, diagnosing susceptibility to a disease which is caused
CC by toxins or procarcinogens metabolized by CYP3A5 and for identifying
CC mutagenic effects of a compound
XX
SQ Sequence 16 BP; 6 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTACGTGTAC 16
|| | |||||
Db 11 CTCCCTGTAC 2

RESULT 662
AAT77699
ID AAT77699 standard; DNA; 19 BP.
XX
AC AAT77699;
XX
DT 15-SEP-1997 (first entry)
XX
DE Wheat microsatellite WMS261 left primer.
XX
KW Microsatellite marker; hypervariable genomic fragment; Triticum aestivum;
KW wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify;
KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
XX
OS Synthetic.
XX
PN DE19525284-A1.
XX
PD 02-JAN-1997.
XX
PF 28-JUN-1995; 95DE-01025284.
XX
PR 28-JUN-1995; 95DE-01025284.
XX
PA (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.
XX
PI Roeder M, Plaschke J, Ganal M;
XX
DR WPI; 1997-053731/06.
XX
PT Primers for STS micro:satellite markers for wheat and related species -
PT useful for genetic mapping, analysis and labelling etc. of wheat.
XX
PS Claim 5; Page 8; 8pp; German.
XX
CC Microsatellite markers based on hypervariable genomic fragments, from
CC Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence
CC tagged site (STS), defined by 2 specific primers (of mean size 17-23
CC bases) that flank a microsatellite sequence at both ends, which can be
CC amplified to polymorphisms (PCR products of different sizes). The
CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-
CC or tetra-nucleotide sequences, combination microsatellite sequences or an
CC imperfect sequence in which individual bases are mutated. The
CC microsatellite markers can be used for genetic analysis of hexaploid and
CC tetraploid forms of wheat and for genetic mapping or labelling of
CC monogenic and polygenic properties, and for their selection; for
CC analysing relationships and identifying varieties; and for evaluating
CC varietal purity, hybrid identification and plant growth. The markers can
CC differentiate between almost all European wheat lines and show a higher
CC degree of DNA polymorphism than known probes for the wheat genome. They
CC can be detected by PCR, so large numbers of samples can be analysed
CC easily (e.g. several hundred per day). Microsatellite marker-related
CC polymorphisms are stably inherited so can also serve as genetic markers.
CC AAT77003-22 and AAT77535-716 are primer pairs that define the
CC microsatellite markers. WMS261 has a CT type repeat
XX
SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTACGTGTAC 16
|| | |||||
Db 1 CTCCCTGTAC 10

RESULT 663
ADB01852/c
ID ADB01852 standard; DNA; 25 BP.
XX
AC ADB01852;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 2838.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 2838; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 25;
Best Local Similarity 61.1%; Pred. No. 5.8e+02;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          5 CCCTACGTGTACAGGGAG 22
              | ||    || ||| | ||
Db         25 CACTCGCTGCACACGTAG 8
```

RESULT 664
AAV11022/c
ID AAV11022 standard; RNA; 13 BP.
XX
AC AAV11022;
XX
DT 25-MAR-2003 (revised)
DT 14-JUL-1998 (first entry)
XX
DE Human ribozyme target sequence from HLA-DPB 02DPB #3.
XX
KW Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
KW major histocompatability complex; cleavage; suppression; transplant;
KW incompatibility; autoimmune disease; juvenile diabetes;
KW rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9704087-A1.
XX
PD 06-FEB-1997.
XX
PF 18-JUL-1996; 96WO-EP003173.
XX
PR 18-JUL-1995; 95EP-00111256.
XX
PA (KRUP/) KRUPP G.
PA (MARG/) MARGET M.
PA (WEST/) WESTPHAL E.
PA (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;
XX
DR WPI; 1997-132628/12.
XX
PT Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT versus host reactions, to overcome blood incompatibility and to treat
PT auto:immune disease.
XX
PS Claim 5; Fig 1; 76pp; German.
XX
CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC specific alleles from the major histocompatability complex (MHC). This
CC ribozyme contains a catalytic region and a hybridisation region which is
CC complementary to all mRNA transcribed from vertebrate genes of a specific
CC family of closely related MHC alleles or to mRNA from a single MHC
CC allele, and is able to cleave such mRNA. The mRNA has a target region
CC which in case is essentially conserved in all genes of the family but
CC differs from genes of all other MHC alleles to such a degree that no
CC cleavage of mRNA transcribed from these other alleles occurs. This allows
CC the selective reduction or inhibition of expression of all genes of a
CC family or of a single gene. This ribozyme can be used for permanent or
CC transient suppression of expression of MHC alleles, in vivo or in vitro.
CC Specific applications are to prevent guest vs. host or host vs. guest
CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC and Kell systems) and to treat autoimmune diseases such as juvenile
CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC need for immunosuppressants in transplant patients. It provides very
CC specific reduction of particular HLA molecules that cause incompatibility
CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 13 BP; 3 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

```
  Query Match             23.6%;  Score 6.6;  DB 1;  Length 13;
  Best Local Similarity   69.2%;  Pred. No. 6.3e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          9 ACGTGTACAGGGA 21
              ||  ||||| | |
Db         13 ACTGGTACACGTA 1
```

RESULT 665
AAF47953
ID AAF47953 standard; DNA; 15 BP.
XX
AC AAF47953;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1373.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 53; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             23.6%;  Score 6.6;  DB 1;  Length 15;
  Best Local Similarity   69.2%;  Pred. No. 6.9e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          5 CCCTACGTGTACA 17
              | || |  |||||
Db          3 CACTCCCCGTACA 15
```

```
RESULT 666
AAQ99935/c
ID   AAQ99935 standard; DNA; 16 BP.
XX
AC   AAQ99935;
XX
DT   07-MAY-1996  (first entry)
XX
DE   Human MTS1 RT-PCR primer, X2B.
XX
KW   Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;
KW   astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW   gene therapy; chronic; ss.
XX
OS   Homo sapiens.
XX
PN   WO9525429-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;   95WO-US003316.
XX
PR   18-MAR-1994;   94US-00214581.
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215088.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1995-344401/44.
XX
PT   Wild-type multiple tumour suppressor (MTS) gene and mutant sequences -
PT   useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma
PT   or leukaemia.
XX
PS   Example 12; Page 68; 156pp; English.
XX
CC   The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC   polypeptides have been isolated and sequenced, using various sequencing
CC   and amplification primers. The primer represented in this sequence was
CC   used to distinguish between two different promoters of MTS1, one alpha-
CC   specific and one beta-specific. MTS polypeptide-encoding cDNAs and
CC   mutants of these are useful for the diagnosis or prognosis of human
CC   cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing
CC   predisposition to melanoma, leukaemia, astrocytoma, glioblastoma,
CC   lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas,
CC   thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type
CC   gene is useful for gene therapy and MTS polypeptides may also be used for
CC   protein replacement therapy. Also the polypeptides or cells contg. an
CC   altered MTS gene are useful for screening for potential cancer
CC   therapeutics
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 667
AAT00727/c
ID   AAT00727 standard; DNA; 16 BP.
XX
AC   AAT00727;
XX
DT   08-MAY-1996  (first entry)
XX
DE   Multiple tumour suppressor 1 gene PCR primer.
XX
KW   Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW   predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas;
KW   breast; thyroid; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9525813-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;   95WO-US003537.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Skolnick MH,  Cannon-Albright LA,  Kamb A;
XX
DR   WPI; 1995-344626/44.
XX
PT   Detecting polymorphism associated with cancer pre:disposition - also DNA,
PT   vectors and host cells e.g. for gene or protein replacement therapy and
PT   drug screening.
XX
PS   Example 12; Page 68; 148pp; English.
XX
CC   An individual can be diagnosed as having a predisposition to cancer by
CC   detecting an alteration in the wild type multiple tumour suppressor (MTS)
CC   gene, using gene probes which hybridise to the MTS1 gene exon 1 or exon
CC   1beta (amplified using the PCR primers AAT00724-27). The above assay can
CC   also be used in the diagnosis and prognosis of melanoma, lymphoma,
CC   leukaemia and pancreas, breast and thyroid cancers, etc
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 668
AAT69788/c
ID   AAT69788 standard; DNA; 16 BP.
XX
AC   AAT69788;
XX
DT   25-MAR-2003  (revised)
DT   10-SEP-1997  (first entry)
XX
DE   P16 promoter primer X2B.
XX
KW   Primer; polymerase chain reaction; PCR; amplification; P16; promoter; ss.
XX
OS   Synthetic.
XX
PN   US5624819-A.
XX
PD   29-APR-1997.
XX
PF   07-JUN-1995;   95US-00474177.
```

```
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003537.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Cannon-Albright LA,  Kamb A,  Skolnick MH;
XX
DR   WPI; 1997-258217/23.
XX
PT   Human mutant multiple tumour suppressor gene sequences - for production
PT   of recombinant mutant polypeptide(s).
XX
PS   Example 12; Col 81-82; 72pp; English.
XX
CC   The present sequence is primer for the PCR amplification of the P16
CC   promoter. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 669
AAV53838/c
ID   AAV53838 standard; DNA; 16 BP.
XX
AC   AAV53838;
XX
DT   04-DEC-1998  (first entry)
XX
DE   Nucleotide sequence of PCR primer 9.
XX
KW   Multiple tumour suppressor; MTS; human; cancer; hybridisation;
KW   somatic mutation; gene therapy; PCR; primer; amplification; ss.
XX
OS   Synthetic.
XX
PN   US5801236-A.
XX
PD   01-SEP-1998.
XX
PF   07-JUN-1995;   95US-00480810.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1998-494842/42.
XX
PT   Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT   useful as hybridisation probes, primers and recombinant production of MTS
PT   in the diagnosis and treatment of cancers related to MTS mutation(s).
XX
PS   Example 12; Col 51; 73pp; English.
XX
CC   This is the nucleotide sequence of a PCR primer used for amplification in
CC   the method of the invention involving the used of the multiple tumour
CC   suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is
CC   useful in the diagnosis and prognosis of human cancer, e.g. by standard
CC   nucleic hybridisation techniques, of patient samples. The mutated
CC   sequences are those that are present in somatic mutations of the gene in
CC   cancers. The vectors can be used for gene therapy strategies to replace
CC   function of mutated protein in patients. These can also be used to
CC   construct protein mimetics, also for therapeutic strategies. In addition
CC   the expression constructs can also be used for recombinant production of
CC   MTS. Recombinant MTS can be used to screen for drugs to be used for
CC   cancer therapy, and the protein itself may also be used to restore MTS
CC   function in a cell
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 670
AAV11257/c
ID   AAV11257 standard; DNA; 16 BP.
XX
AC   AAV11257;
XX
DT   15-JUL-1998  (first entry)
XX
DE   Human MTS1 and MTS1E1-beta PCR primer X2B.
XX
KW   MTS1; MTS2; multiple tumour suppressor; diagnosis; cancer;
KW   germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5739027-A.
XX
PD   14-APR-1998.
XX
PF   07-JUN-1995;   95US-00487033.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1998-250421/22.
XX
PT   DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful
PT   for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their
PT   treatment.
XX
PS   Example 12; Col 81-82; 72pp; English.
XX
CC   Primers AAV11256 and AAV11257 are used in the isolation of the human
CC   multiple tumour suppression proteins, MTS1 and MTS1E1-beta. The MTS gene
CC   locus is also referred to as the familial melanoma (MLM) gene locus,
CC   located on human chromosome 9p21. Germ line mutations in MTS genes can be
CC   used in the diagnosis of predisposition to cancers, e.g. melanoma,
CC   leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
```

```
CC   lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1

RESULT 671
AAV70602/c
ID   AAV70602 standard; DNA; 16 BP.
XX
AC   AAV70602;
XX
DT   20-MAR-2003  (revised)
DT   03-FEB-1999  (first entry)
XX
DE   PCR primer X2B for multiple tumour suppressor 2 gene.
XX
KW   Human; multiple tumour suppressor 2 gene; MTS2; cancer; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5843756-A.
XX
PD   01-DEC-1998.
XX
PF   28-JUL-1995;   95US-00508735.
XX
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00487033.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Jiang P,  Kamb A,  Stone S;
XX
DR   WPI; 1999-044585/04.
XX
PT   Mouse multiple tumour suppressor gene segment - useful for primer design.
XX
PS   Example 14; Col 54; 80pp; English.
XX
CC   PCR primers AAV70600-02 were used to amplify a human multiple tumour
CC   suppressor 2 (MTS2) gene. The MTS2 gene nucleotide sequence can be used
CC   to design primers to detect abnormalities i.e. polymorphisms which may
CC   predispose towards malignancies such as melanoma, leukaemia, astrocytoma,
CC   lymphoma, glioma, as well as tumours of e.g. the breast, thyroid,
CC   pancreas, uterus and kidneys. (Updated on 20-MAR-2003 to correct PF
CC   field.) (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1

RESULT 672
AAA95654/c
ID   AAA95654 standard; DNA; 16 BP.
XX
AC   AAA95654;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Human P16 promoter beta-specific primer X2B.
XX
KW   Cytostatic; human; multiple tumour suppressor 2; MTS2; diagnostic;
KW   cancer; gene therapy; protein replacement therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6090578-A.
XX
PD   18-JUL-2000.
XX
PF   08-DEC-1997;   97US-00986515.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-514036/46.
XX
PT   Novel protein composition useful in protein replacement therapy for
PT   diagnosing and treating cancer comprises a specific weight percent of
PT   human multiple tumor suppressor 1 polypeptide.
XX
PS   Example 12; Col 49; 72pp; English.
XX
CC   The invention relates to the isolation of the gene encoding the human
CC   multiple tumour suppressor 1 (MTS1) (AAA95633). The MTS1 protein has a
CC   cytostatic activity and is used in protein replacement therapy. This
CC   sequence is a PCR primer used in the amplification of the beta-specific
CC   form of the P16 promoter. MTS1 is useful in diagnosing human cancers such
CC   as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
CC   glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
CC   cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
CC   pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
CC   uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
CC   useful in gene therapy, protein replacement therapy and protein mimetic
CC   studies
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1

RESULT 673
AAZ48793/c
ID   AAZ48793 standard; cDNA; 16 BP.
XX
AC   AAZ48793;
XX
DT   21-MAR-2000  (first entry)
XX
DE   PCR primer for human MTS1E1beta coding sequence.
XX
KW   MTS; human; polymorphism detection; cancer predisposition; astrocytoma;
KW   Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;
KW   lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;
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KW   therapy; MTS1E1beta; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US5989815-A.
XX
PD   23-NOV-1999.
XX
PF   29-APR-1997;   97US-00848251.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003537.
PR   07-JUN-1995;   95US-00474083.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Skolnick MH,  Cannon-Albright LA,  Kamb A;
XX
DR   WPI; 2000-070785/06.
XX
PT   Diagnosing a polymorphism associated with a predisposition for cancer.
XX
PS   Example 12; Col 48; 74pp; English.
XX
CC   This sequence is a PCR primer for DNA encoding human MTS1E1beta. The
CC   invention relates to a method for diagnosing a polymorphism associated
CC   with a predisposition to cancer by detecting a germ-line alteration of a
CC   wild-type Multiple Tumour Suppressor (MTS) gene or its expression
CC   products in a human sample. The method comprises detecting a germ-line
CC   alteration of a wild-type MTS gene or its expression products in a human
CC   sample, the alteration indicating a predisposition to at least one of the
CC   cancers. The cancer is selected from melanoma, leukaemia, astrocytoma,
CC   glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, chronic lymphocytic
CC   leukaemia (CLL), and cancers of the pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum. The method may be used as the
CC   basis for developing very important diagnostic tests capable of
CC   predicting the predisposition to cancer. The MTS gene is involved in the
CC   progression of multiple tumour types and may provide means for a general
CC   anti-cancer therapy by virtue of its ability to suppress tumour growth
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 674
AAZ39993/c
ID   AAZ39993 standard; DNA; 16 BP.
XX
AC   AAZ39993;
XX
DT   11-FEB-2000  (first entry)
XX
DE   PCR primer for human multiple tumour suppressor 1 coding sequence.
XX
KW   Multiple tumour suppressor; MTS2; human; diagnosis; Hodgkin's lymphoma;
KW   cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5994095-A.
XX
PD   30-NOV-1999.
XX
PF   07-JUN-1995;   95US-00486047.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-038259/03.
XX
PT   Multiple tumor suppressor cDNA, useful for diagnosing or determining a
PT   predisposition to cancer.
XX
PS   Example 12; Col 48; 72pp; English.
XX
CC   This sequence represents a PCR primer for the human multiple tumour
CC   suppressor 1 (MTS1) coding sequence. The invention relates to the human
CC   MTS2 DNA and protein sequences. The DNA sequences are useful for
CC   diagnosing or determining a predisposition to cancers e.g. melanoma,
CC   leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the
CC   pancreas, breast, thyroid, ovary, kidney, uterus and stomach
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 675
AAA39372/c
ID   AAA39372 standard; DNA; 16 BP.
XX
AC   AAA39372;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Human P16 PCR primer SEQ ID NO:23.
XX
KW   Human; multiple tumour suppressor; MTS; somatic mutation; cancer;
KW   diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;
KW   leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;
KW   Hodgkin's lymphoma; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6060301-A.
XX
PD   09-MAY-2000.
XX
PF   14-JUL-1998;   98US-00115252.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
PR   08-DEC-1997;   97US-00986147.
```

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XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-349676/30.
XX
PT   New vector useful for gene therapy of cancer associated with mutation in
PT   tumor suppressor gene, comprises DNA sequence of multiple tumor
PT   suppressor gene.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention describes a vector (I) comprising an isolated DNA
CC   sequence of a multiple tumour suppressor (MTS) gene having a
CC   polynucleotide sequence of the human MTS1E1-beta. (I) is useful for
CC   introducing wild-type MTS function to a cancerous or pre-cancerous cell
CC   which carries diminished or mutant MTS alleles for suppressing neoplastic
CC   growth of the recipient cells. (I) is also useful for increasing the
CC   level of expression of MTS gene even in tumour cells in which the mutant
CC   gene is expressed at a normal level but the gene product is not fully
CC   functional. A host cell transformed with (I) is useful as a model system
CC   to study cancer remission and drug treatment which promotes such
CC   remission. The present invention relates to somatic mutations and germ
CC   line mutations in the MTS gene and their use in the diagnosis and
CC   prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma,
CC   glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and cancers of the
CC   pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and
CC   rectum. The present sequence represents a PCR primer used in an example
CC   from the present invention
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 676
AAA11186/c
ID   AAA11186 standard; DNA; 16 BP.
XX
AC   AAA11186;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Human multiple tumour suppressor 1 primer X2B.
XX
KW   Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
KW   cancer; diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6037462-A.
XX
PD   14-MAR-2000.
XX
PF   22-JUL-1998;   98US-00120130.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-269915/23.
XX
PT   New mutants of the human multiple tumor suppressor gene, useful as
PT   diagnostic markers of cancer, contain specific base alterations or
PT   deletions.
XX
PS   Example 12; Col 48; 72pp; English.
XX
CC   The invention relates to variants (AAA11196-A11206) of the human multiple
CC   tumour suppressor 1 (MTS1) gene (AAA11165). The variants have the
CC   following changes relative to this sequence: A at any of positions 265,
CC   442, 330 and 329; T at any of positions 172, 238, 341 and 148 and
CC   deletions of nucleotides 290-294, 172-179 or 128-129. The variants are
CC   somatic mutations of MST1, indicative of predisposition to melanoma and
CC   many other cancers, so detecting them is useful for diagnosis, prognosis
CC   and monitoring of cancer (including prenatal analysis). Cells and animals
CC   that express the variants are useful as model systems for identifying
CC   potential anticancer agents. This sequence represents a primer used to
CC   screen for MTS1 E1beta initial mRNA expression levels
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 677
AAF58190/c
ID   AAF58190 standard; DNA; 16 BP.
XX
AC   AAF58190;
XX
DT   23-APR-2001  (first entry)
XX
DE   Primer #13.
XX
KW   Human; multiple tumour suppressor; MTS; cancer; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   US6180776-B1.
XX
PD   30-JAN-2001.
XX
PF   22-JUL-1998;   98US-00120129.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-158668/16.
XX
PT   Novel multiple tumor suppressor gene useful for diagnosing, prognosing
PT   and treating cancers, such as melanoma, leukemia, glioblastoma and
PT   Hodgkin's lymphoma.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention relates to human multiple tumor suppressor-2 (MTS2)
```

```
AC   AAC83090;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Primer X2B used in the invention.
XX
KW   MTS; Multiple Tumour Suppressor; cancer; antibody; ss.
XX
OS   Homo sapiens.
XX
PN   US6140473-A.
XX
PD   31-OCT-2000.
XX
PF   22-JUL-1998;   98US-00120128.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-014867/02.
XX
PT   New multiple tumor suppressor 2-specific antibodies useful for detecting
PT   differences in the absence of the peptides or mutant gene products, or
PT   for screening tissues.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention relates to an antibody or its fragment that
CC   specifically binds to a human multiple tumour suppressor (MTS). The
CC   invention is useful for detecting differences in the absence of MTS
CC   peptides, to screen a tissue or to detect mutant MTS gene products. The
CC   antibodies will immunoprecipitate MTS proteins from solution as well as
CC   react with MTS protein on Western or immunoblots of polyacrylamide gels
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 681
AAZ79758
ID   AAZ79758 standard; DNA; 10 BP.
XX
AC   AAZ79758;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human breast tumour downregulated gene SAGE tag, SEQ ID NO:49.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 54; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 5.4e+02;
```

```
CC   gene. The invention is useful for diagnosing, prognosing and treating
CC   cancers. It is also useful for screening drugs for cancer therapy and
CC   gene therapy
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 678
AAS02583/c
ID   AAS02583 standard; DNA; 16 BP.
XX
AC   AAS02583;
XX
DT   29-AUG-2001  (first entry)
XX
DE   PCR primer X2B used in analysis of multiple tumour suppressor MTS1/2.
XX
KW   Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; diagnostic;
KW   cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;
KW   lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6210949-B1.
XX
PD   03-APR-2001.
XX
PF   30-NOV-1998;   98US-00201139.
XX
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00487033.
PR   28-JUL-1995;   95US-00508735.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Stone S,  Jiang P,  Kamb A;
XX
DR   WPI; 2001-280859/29.
XX
PT   New mouse multiple tumor suppressor gene, useful for diagnosing or
PT   prognosing human cancer or as gene therapy for treating cancer,
PT   particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the
PT   pancreas or breast.
XX
PS   Example 13; Col 51; 80pp; English.
XX
CC   The sequence represents PCR primer X2B used in analysis of multiple
CC   tumour suppressor MTS1 and MTS2. The MTS genes, and expression products,
CC   are useful for treating, diagnosing or prognosing human cancer. In
CC   particular, the MTS gene is useful for diagnosing a predisposition to or
CC   as a gene therapy for melanoma, leukaemia, astrocytoma, glioblastoma,
CC   lymphoma, glioma, Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL),
CC   or cancers of the pancreas, breast, thyroid, ovary, uterus, testis,
CC   kidney, stomach or rectum. The gene may be used in both cancerous and pre
CC   -cancerous cells
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 679
AAD04711/c
ID   AAD04711 standard; DNA; 16 BP.
XX
AC   AAD04711;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human MTS and MTS1E1beta sequence amplifying primer, X2B.
XX
KW   Human; multiple tumour suppressor; MTS1E1beta; cytostatic;
KW   germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;
KW   glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;
KW   pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;
KW   somatic mutation; MTS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218146-B1.
XX
PD   17-APR-2001.
XX
PF   22-JUL-1998;   98US-00120131.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-289831/30.
XX
PT   Novel multiple tumor suppressor proteins useful for diagnosis and
PT   prognosis of human cancer and for screening drugs for cancer treatment.
XX
PS   Example 13; Col 52; 71pp; English.
XX
CC   The invention relates to somatic and germ line mutations in the multiple
CC   tumour suppressor (MTS) gene in human cancer. The invention also relates
CC   to therapy of human cancer which have a mutation in the MTS gene,
CC   including gene therapy, protein replacement therapy, and protein
CC   mimetics. The MTS sequences are useful for diagnosing predisposition to
CC   human cancer or for diagnosing and prognosing human cancers such as
CC   melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC   Hodgkin's lymphoma, CLL and cancers of pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum. They are also used for
CC   screening drugs for cancer treatment. The present sequence is primer, X2B
CC   used for amplifying human MTS and MTS1E1beta sequence
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             23.6%;  Score 6.6;  DB 1;  Length 16;
  Best Local Similarity   69.2%;  Pred. No. 7e+02;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | || ||| |
Db         13 CTTCCTGGACACG 1


RESULT 680
AAC83090/c
ID   AAC83090 standard; DNA; 16 BP.
XX
```

```
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CGTGTACA 17
              | ||||||
Db          2 CCTGTACA 9


RESULT 682
ABV67783
ID   ABV67783 standard; cDNA; 11 BP.
XX
AC   ABV67783;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5569.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 179; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 11;
  Best Local Similarity   87.5%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CGTGTACA 17
              | ||||||
Db          4 CCTGTACA 11


RESULT 683
ABV70593/c
ID   ABV70593 standard; cDNA; 11 BP.
XX
AC   ABV70593;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8379.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 268; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 11;
  Best Local Similarity   87.5%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||| ||||
Db          8 GGATTCCA 1


RESULT 684
ABV63172/c
ID   ABV63172 standard; cDNA; 11 BP.
XX
AC   ABV63172;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 958.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
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XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 51; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 11;
  Best Local Similarity   87.5%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||| ||||
Db          8 GGATTCCA 1


RESULT 685
ABV70819/c
ID   ABV70819 standard; cDNA; 11 BP.
XX
AC   ABV70819;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8605.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 275; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 11;
  Best Local Similarity   87.5%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CGTGTACA 17
              | ||||||
Db         11 CCTGTACA 4


RESULT 686
ABV63398/c
ID   ABV63398 standard; cDNA; 11 BP.
XX
AC   ABV63398;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1184.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 57; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
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CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 11;
  Best Local Similarity   87.5%;  Pred. No. 6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CGTGTACA 17
              | ||||||
Db         11 CCTGTACA 4


RESULT 687
ABH73583
ID   ABH73583 standard; DNA; 12 BP.
XX
AC   ABH73583;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273568 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273568; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 12;
  Best Local Similarity   87.5%;  Pred. No. 6.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db          3 TACGCGTA 10


RESULT 688
ABI10705/c
ID   ABI10705 standard; DNA; 12 BP.
XX
AC   ABI10705;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310678 for detecting SNP TSC0024049.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 310678; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 12;
  Best Local Similarity   87.5%;  Pred. No. 6.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db         11 TACGCGTA 4


RESULT 689
ABI16213/c
ID   ABI16213 standard; DNA; 12 BP.
XX
AC   ABI16213;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

```
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 12;
  Best Local Similarity   87.5%;  Pred. No. 6.5e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              |||||| |
Db          8 CCCTACTT 1


RESULT 690
ABC49804
ID   ABC49804 standard; DNA; 13 BP.
XX
AC   ABC49804;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 49821 for detecting SNP TSC0014053.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 49821; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 13;
  Best Local Similarity   87.5%;  Pred. No. 6.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db          3 TACGCGTA 10


RESULT 691
ABC49805/c
ID   ABC49805 standard; DNA; 13 BP.
XX
AC   ABC49805;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 49822 for detecting SNP TSC0014053.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
```

```
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 1 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 13;
  Best Local Similarity   87.5%;  Pred. No. 6.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db         11 TACGCGTA 4


RESULT 692
ABC37725
ID   ABC37725 standard; DNA; 13 BP.
XX
AC   ABC37725;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37742 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37742; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 13;
  Best Local Similarity   87.5%;  Pred. No. 6.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db          5 TACGCGTA 12


RESULT 693
ABC37724/c
ID   ABC37724 standard; DNA; 13 BP.
XX
AC   ABC37724;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37741 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37741; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 13;
  Best Local Similarity   87.5%;  Pred. No. 6.8e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTA 15
              |||| |||
Db          9 TACGCGTA 2


RESULT 694
ADB00353/c
ID   ADB00353 standard; DNA; 17 BP.
```

```
XX
AC   ADB00353;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1339.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1339; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   62.5%;  Pred. No. 7.4e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              ||   || ||| | ||
Db         17 CTCGCTGCACACGTAG 2


RESULT 695
ADB00354/c
ID   ADB00354 standard; DNA; 17 BP.
XX
AC   ADB00354;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1340.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1340; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   62.5%;  Pred. No. 7.4e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              ||   || ||| | ||
Db         16 CTCGCTGCACACGTAG 1


RESULT 696
ADB00356/c
ID   ADB00356 standard; DNA; 17 BP.
XX
AC   ADB00356;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1342.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
```

```
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1342; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   62.5%;  Pred. No. 7.4e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGG 19
              || ||   || ||| |
Db         17 GCACTCGCTGCACACG 2


RESULT 697
ADB00357/c
ID   ADB00357 standard; DNA; 17 BP.
XX
AC   ADB00357;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1343.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1343; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 17;
  Best Local Similarity   62.5%;  Pred. No. 7.4e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGG 19
              || ||   || ||| |
Db         16 GCACTCGCTGCACACG 1


RESULT 698
ADB01851/c
ID   ADB01851 standard; DNA; 25 BP.
XX
AC   ADB01851;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2837.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
```

XX
PS Example 8; SEQ ID NO 2837; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

```
  Query Match             22.9%;  Score 6.4;  DB 1;  Length 25;
  Best Local Similarity   62.5%;  Pred. No. 5.9e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              ||   || ||| | ||
Db         24 CTCGCTGCACACGTAG 9
```

RESULT 699
ADB01850/c
ID ADB01850 standard; DNA; 25 BP.
XX
AC ADB01850;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 2836.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 2836; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

```
  Query Match             22.9%;  Score 6.4;  DB 1;  Length 25;
  Best Local Similarity   62.5%;  Pred. No. 5.9e+02;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              ||   || ||| | ||
Db         25 CTCGCTGCACACGTAG 10
```

RESULT 700
ABI00908
ID ABI00908 standard; DNA; 12 BP.
XX
AC ABI00908;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 300881 for detecting SNP TSC0019231.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 300881; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

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  Query Match             22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          2 CTCCCTCTACA 12


RESULT 701
ABI54047
ID   ABI54047 standard; DNA; 12 BP.
XX
AC   ABI54047;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 354020 for detecting SNP TSC0048852.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 354020; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          1 CTCCCTCTACA 11


RESULT 702
ABI21821
ID   ABI21821 standard; DNA; 12 BP.
XX
AC   ABI21821;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 321794 for detecting SNP TSC0030495.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 321794; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          1 CTCCCTATACA 11


RESULT 703
ABH71301/c
ID   ABH71301 standard; DNA; 12 BP.
XX
AC   ABH71301;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 271278 for detecting SNP TSC0002450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
```

```
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 271278; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||| | | ||
Db          12 TGTATACGAAG 2


RESULT 704
ABI37455/c
ID   ABI37455 standard; DNA; 12 BP.
XX
AC   ABI37455;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 337428 for detecting SNP TSC0039870.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTACA 17
               || | | ||||
Db          11 CTCCTTCTACA 1


RESULT 705
ABI72643
ID   ABI72643 standard; DNA; 12 BP.
XX
AC   ABI72643;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 372616 for detecting SNP TSC0059501.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 372616; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
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CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          2 CTCCATATACA 12


RESULT 706
ABH72448/c
ID   ABH72448 standard; DNA; 12 BP.
XX
AC   ABH72448;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 272433 for detecting SNP TSC0002816.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 272433; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
                ||||  | | ||
Db         12 TGTATATGTAG 2


RESULT 707
ABI22910/c
ID   ABI22910 standard; DNA; 12 BP.
XX
AC   ABI22910;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 322883 for detecting SNP TSC0031094.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 322883; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match            22.1%;  Score 6.2;  DB 1;  Length 12;
  Best Local Similarity   72.7%;  Pred. No. 7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||| | | |||
Db         12 CCTCCCTCTAC 2


RESULT 708
ABF18028
ID   ABF18028 standard; DNA; 13 BP.
XX
AC   ABF18028;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118025 for detecting SNP TSC0029509.
```

```
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118025; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              ||||  | | ||
Db          1 TGTAGAAGTAG 11


RESULT 709
ABF18029/c
ID   ABF18029 standard; DNA; 13 BP.
XX
AC   ABF18029;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118026 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118026; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
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CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              ||||  | | ||
Db         13 TGTAGAAGTAG 3


RESULT 710
ABC90236/c
ID   ABC90236 standard; DNA; 13 BP.
XX
AC   ABC90236;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 90253 for detecting SNP TSC0022616.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 90253; 29pp + Sequence Listing; German.
```

```
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAGT 23
               ||||| | | |
Db          12 GTACACGTATT 2


RESULT 711
ABC90237
ID   ABC90237 standard; DNA; 13 BP.
XX
AC   ABC90237;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 90254 for detecting SNP TSC0022616.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 90254; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAGT 23
               ||||| | | |
Db           2 GTACACGTATT 12


RESULT 712
ABF36729
ID   ABF36729 standard; DNA; 13 BP.
XX
AC   ABF36729;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136726 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136726; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTACA 17
               || | | ||||
Db           3 CTCCATTTACA 13


RESULT 713
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```
ABF60519
ID   ABF60519 standard; DNA; 13 BP.
XX
AC   ABF60519;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160516 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160516; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          1 CTCCTTCTACA 11


RESULT 714
ABF60516/c
ID   ABF60516 standard; DNA; 13 BP.
XX
AC   ABF60516;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160513 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160513; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db         13 CTCCTTTTACA 3


RESULT 715
ABC56486
ID   ABC56486 standard; DNA; 13 BP.
XX
AC   ABC56486;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 56503 for detecting SNP TSC0015314.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
```

```
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 56503; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              ||| | | |||
Db          2 GTAAACGTAGT 12


RESULT 716
ABF82918
ID   ABF82918 standard; DNA; 13 BP.
XX
AC   ABF82918;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 182915 for detecting SNP TSC0045193.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 182915; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| | | ||
Db          2 TGTATATGTAG 12


RESULT 717
ABF36728/c
ID   ABF36728 standard; DNA; 13 BP.
XX
AC   ABF36728;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136725 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136725; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
```

```
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db         11 CTCCATTTACA 1


RESULT 718
ABF20036
ID   ABF20036 standard; DNA; 13 BP.
XX
AC   ABF20036;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120033 for detecting SNP TSC0029958.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120033; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| | | ||
Db          2 TGTAAAAGTAG 12


RESULT 719
ABF60517
ID   ABF60517 standard; DNA; 13 BP.
XX
AC   ABF60517;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160514 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160514; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | | ||||
Db          1 CTCCTTTTACA 11


RESULT 720
ABF20037/c
ID   ABF20037 standard; DNA; 13 BP.
XX
AC   ABF20037;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120034 for detecting SNP TSC0029958.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
```

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XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120034; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||| | | ||
Db          12 TGTAAAAGTAG 2


RESULT 721
ABF60518/c
ID   ABF60518 standard; DNA; 13 BP.
XX
AC   ABF60518;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160515 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160515; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTACA 17
               || | | ||||
Db          13 CTCCTTCTACA 3


RESULT 722
ABC56487/c
ID   ABC56487 standard; DNA; 13 BP.
XX
AC   ABC56487;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 56504 for detecting SNP TSC0015314.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 56504; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
```

```
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              ||| | | |||
Db         12 GTAAACGTAGT 2


RESULT 723
ABF82919/c
ID   ABF82919 standard; DNA; 13 BP.
XX
AC   ABF82919;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 182916 for detecting SNP TSC0045193.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 182916; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 13;
  Best Local Similarity   72.7%;  Pred. No. 7.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| | | ||
Db         12 TGTATATGTAG 2


RESULT 724
AAF46048
ID   AAF46048 standard; DNA; 15 BP.
XX
AC   AAF46048;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #887.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 15;
  Best Local Similarity   72.7%;  Pred. No. 7.7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | || |||
Db          2 CTCCCTGCACA 12


RESULT 725
AAF46045
```

```
ID   AAF46045 standard; DNA; 15 BP.
XX
AC   AAF46045;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #884.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 15;
  Best Local Similarity   72.7%;  Pred. No. 7.7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | || |||
Db          5 CTCCCTGCACA 15


RESULT 726
AAF46046
ID   AAF46046 standard; DNA; 15 BP.
XX
AC   AAF46046;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #885.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 15;
  Best Local Similarity   72.7%;  Pred. No. 7.7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | || |||
Db          4 CTCCCTGCACA 14


RESULT 727
AAF46047
ID   AAF46047 standard; DNA; 15 BP.
XX
AC   AAF46047;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #886.
XX
```

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 39; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACA 17
|| | || |||
Db 3 CTCCCTGCACA 13

RESULT 728
AAT54219/c
ID AAT54219 standard; RNA; 15 BP.
XX
AC AAT54219;
XX
DT 25-MAR-2003 (revised)
DT 24-MAR-1997 (first entry)
XX
DE Human IL-5 hammerhead ribozyme target sequence (nt. position 91).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9523225-A2.
XX
PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 214; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
CC of the mRNA that do not form secondary folding structures and that
CC contain potential hammerhead and hairpin ribozyme cleavage sites were
CC identified by computer analysis. Ribozymes directed against these mRNA
CC sequences were designed and synthesised with modifications that improve
CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
CC and thereby inhibit IL-5 expression, making them useful for treating
CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
CC and preventing the recruitment and activation of eosinophils. The
CC ribozymes can also be used to treat eosinophilia (related to parasitic
CC infection or with pulmonary infiltration) and L-tryptophan-associated
CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
CC field.)

```
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 15;
  Best Local Similarity   72.7%;  Pred. No. 7.7e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTC 24
              |||| | || |
Db         14 TACACGTAGGC 4


RESULT 729
ADB00349/c
ID   ADB00349 standard; DNA; 17 BP.
XX
AC   ADB00349;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1335.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1335; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 17;
  Best Local Similarity   72.7%;  Pred. No. 7.6e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
                 || ||| | ||
Db         16 TGCACACGTAG 6


RESULT 730
ADB00350/c
ID   ADB00350 standard; DNA; 17 BP.
XX
AC   ADB00350;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1336.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1336; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 17;
  Best Local Similarity   72.7%;  Pred. No. 7.6e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
                 || ||| | ||
Db         15 TGCACACGTAG 5


RESULT 731
ADB00352/c
ID   ADB00352 standard; DNA; 17 BP.
XX
```

AC ADB00352;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 1338.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 1338; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAG 22
|| ||| | ||
Db 13 TGCACACGTAG 3

RESULT 732
ADB00351/c
ID ADB00351 standard; DNA; 17 BP.
XX
AC ADB00351;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 1337.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 1337; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAG 22
|| ||| | ||
Db 14 TGCACACGTAG 4

RESULT 733
ADB00348/c
ID ADB00348 standard; DNA; 17 BP.
XX
AC ADB00348;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 1334.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.

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XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1334; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             22.1%;  Score 6.2;  DB 1;  Length 17;
  Best Local Similarity   72.7%;  Pred. No. 7.6e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              || ||| | ||
Db         17 TGCACACGTAG 7


RESULT 734
ABQ72155
ID   ABQ72155 standard; DNA; 9 BP.
XX
AC   ABQ72155;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2453.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 62; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCC 7
              ||||||
Db          3 GGGCCC 8


RESULT 735
ABQ72156
ID   ABQ72156 standard; DNA; 9 BP.
XX
AC   ABQ72156;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2454.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
```

```
XX
PS   Example 1; Page 62; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCC 7
              ||||||
Db          3 GGGCCC 8


RESULT 736
ADA64482
ID   ADA64482 standard; DNA; 9 BP.
XX
AC   ADA64482;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #940.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 27; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCC 7
              ||||||
Db          3 GGGCCC 8


RESULT 737
ADA64483
ID   ADA64483 standard; DNA; 9 BP.
XX
AC   ADA64483;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #941.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 27; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 6;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GGGCCC 7
              ||||||
Db          3 GGGCCC 8
```

Search completed: April 19, 2004, 15:00:31
Job time : 4 secs